

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 15:10:14 ; Search time 156 Seconds  
(without alignments)  
1027.897 Million cell updates/sec

Title: US-09-879-248-6  
Perfect score: 2310  
Sequence: 1 MSILILNNTSSPGLFQSG.....LGDVENHYKVPMSANLKVAE 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2310	100.0	447	AAW96260	Hypersens
2	2310	100.0	447	AAW71094	Erwinia a
3	2310	100.0	447	AAW84855	A hyperse
4	2310	100.0	447	Aao22548	Hypersens
5	2310	100.0	447	AAE18296	Erwinia a
6	2310	100.0	447	AAE16448	E. amylov
7	2310	100.0	447	ABO9226	Erwinia a
8	559	24.2	424	AAW97851	Hypersens
9	559	24.2	424	AAW71098	Pseudomon
10	559	24.2	424	AAW83014	Pseudomon
11	559	24.2	424	AAW84859	A hyperse
12	559	24.2	424	AAO22550	Hypersens
13	559	24.2	424	AAE18298	Pseudomon
14	559	24.2	424	AAE16452	P. syring
15	359.5	15.6	197	AAW809228	P. syring
16	359.5	15.6	197	AAW83014	Bacillus
17	341	14.8	221	AAW77412	Bacillus
18	341	14.8	221	AAW28446	Bacillus
19	199.5	8.6	1306	ADK48880	Bacillus
20	193	8.4	694	ABU36481	Protein e
21	191.5	8.3	584	ABU36802	Protein e
22	191	8.3	2280	ABU22680	Protein e
23	188	8.1	639	ABU36685	Protein e
24	186.5	8.1	591	ABU36439	Protein e
25	185.5	8.0	1381	ABU36971	Protein e

26	185	8.0	588	7	ADM40790	Adm40790 Mycobacte
27	183	7.9	588	6	ABU36945	Protein e
28	182	7.9	606	6	ABU36540	Protein e
29	181.5	7.9	484	6	ABU15873	Mycobacte
30	181.5	7.9	484	6	ABU36943	Protein e
31	181.5	7.9	484	7	ABO23518	Mycobacte
32	181.5	7.9	2411	3	ABO23860	Haemophil
33	180.5	7.8	1079	7	ABO23519	Mycobacte
34	179	7.7	730	3	AAO29582	Arabidops
35	179	7.7	752	3	AAO29581	Arabidops
36	176.5	7.6	562	6	ABU36590	Protein e
37	176.5	7.6	2090	4	ABB64682	Drosophil
38	174	7.5	615	6	ABU36862	Protein e
39	174	7.5	2042	2	AAW56319	Haemophil
40	174	7.5	2586	4	ABB66878	Drosophil
41	172.5	7.5	584	6	ABU36979	Protein e
42	171.5	7.4	667	6	ABU36570	Protein e
43	171	7.4	505	6	ABU34417	Protein e
44	169.5	7.3	914	6	ABU36682	Protein e
45	169	7.3	525	6	ABU36839	Protein e

## ALIGNMENTS

RESULT 1  
AAW96260  
ID AAW96260 standard; protein; 447 AA.  
XX  
AC AAW96260;  
XX  
DT 14-JUN-1999 (first entry)  
XX  
DE Hypersensitive response eliciting protein (HrpW).  
XX  
KW Hypersensitive response elicitor protein; hypersensitive response; hrpW;  
KW pathogen; infection; crop protection; disease resistance;  
KW pest resistance; transgenic plant; colouration; maturation.  
XX  
OS Erwinia amylovora.  
XX  
PN WO9907208-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 27-JUL-1998; 98MO-US015547.  
XX  
PR 06-AUG-1997; 97US-0055108P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Kim JF, Beer SV;  
XX  
DR WPI; 1999-167126/14.  
XX  
N-PSDB; AAX09007.  
XX  
PT New Erwinia amylovora hypersensitive response eliciting gene and protein  
PT - useful for providing transgenic plants and seeds with enhanced growth,  
XX and insect and disease resistance.  
XX  
PS Claim 1; Page 50-51; 54pp; English.  
XX  
CC The hypersensitive response eliciting protein (hrp) or polypeptide is  
CC produced as part of an active defense by plants against incompatible  
CC pathogen infections. The hypersensitive response is a rapid localised  
CC necrosis. The hrp protein and gene when used in nucleotide constructs are  
CC useful for providing disease resistance to plants, insect control to  
CC plants, and enhancing plant growth (enhancing fruit size and earlier  
CC colouration and maturation), by direct application of the protein to  
XX plants, or by producing transgenic plants or seeds using the hrp gene  
XX Sequence 447 AA;  
SQ

```

Query Match      100.0%; Score 2310; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
DB 1 MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
QY 61 POSGNAATGAGNDQTTGVGNAGLNGRKGTAGTTTPOSQSNMLSEMGNGGLDQAITPDG 120
DB 61 POSGNAATGAGNDQTTGVGNAGLNGRKGTAGTTTPOSQSNMLSEMGNGGLDQAITPDG 120
QY 121 QGGGQIGDNPLLKAMLLIARMWDGSDQFGQPGTGNNSASGTSSSGSGSPFNDLSGGKA 180
DB 121 QGGGQIGDNPLLKAMLLIARMWDGSDQFGQPGTGNNSASGTSSSGSGSPFNDLSGGKA 180
QY 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDPPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
DB 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDPPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGQSGSEKQKPLFILEDGAS 300
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGQSGSEKQKPLFILEDGAS 300
QY 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGDAITVKPNSAGKXSHVEITNSSFEHASD 360
DB 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGDAITVKPNSAGKXSHVEITNSSFEHASD 360
QY 361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
DB 361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 3
AAY84855
ID AAY84855 standard; protein; 447 AA.
XX AC AAY84855;
XX DT 08-AUG-2000 (first entry)
XX DE A hypersensitive response elicitor protein.
XX DE Hypersensitive response; insect control; disease resistance;
XX KW Hypersensitive response elicitor; plant growth; vegetable; crop;
XX KW ornamental plant.
XX OS Erwinia amylovora.
XX PN WO200020452-A2.
XX PD 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US023181.
XX PR 05-OCT-1998; 98US-0103050P.
XX PA (EDEN-) EDEN BIOSCIENCE CORP.
XX PI Wei Z, Fan H, Niggemeyer JL;
XX WPI; 2000-303745/26.
XX DR
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Query Match      100.0%; Score 2310; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
DB 1 MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
QY 61 POSGNAATGAGNDQTTGVGNAGLNGRKGTAGTTTPOSQSNMLSEMGNGGLDQAITPDG 120
DB 61 POSGNAATGAGNDQTTGVGNAGLNGRKGTAGTTTPOSQSNMLSEMGNGGLDQAITPDG 120
QY 121 QGGGQIGDNPLLKAMLLIARMWDGSDQFGQPGTGNNSASGTSSSGSGSPFNDLSGGKA 180
DB 121 QGGGQIGDNPLLKAMLLIARMWDGSDQFGQPGTGNNSASGTSSSGSGSPFNDLSGGKA 180
QY 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDPPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
DB 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDPPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGQSGSEKQKPLFILEDGAS 300
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGQSGSEKQKPLFILEDGAS 300
QY 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGDAITVKPNSAGKXSHVEITNSSFEHASD 360
DB 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGDAITVKPNSAGKXSHVEITNSSFEHASD 360
QY 361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
DB 361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 2
AAY71094
ID AAY71094 standard; protein; 447 AA.
XX AC AAY71094;
XX DT 08-SEP-2000 (first entry)
XX DE Erwinia amylovora hypersensitive response elicitor #2.
XX KW Hypersensitive response elicitor; environmental stress resistance; plant.
XX OS Erwinia amylovora.
XX PN WO200028055-A2.
XX PD 18-MAY-2000.
XX PF 04-NOV-1999; 99WO-US026039.
XX PR 05-NOV-1998; 98US-0107243P.
XX PA (EDEN-) EDEN BIOSCIENCE CORP.
XX PI Wei Z, Schading RL;
XX WPI; 2000-376566/32.
XX N-PSDB; AAD00669.
XX Application of a hypersensitive response elicitor protein to plants to
XX impart stress resistance.
XX Disclosure; Page 10-12; 84pp; English.
XX The patent discloses a method to impart stress resistance to plants by
XX applying a hypersensitive response elicitor in a non-infectious form to a
XX CC
```

DR N-PSDB; AAL4939.  
XX Hypersensitive response elicitor polypeptides useful for imparting  
PT enhanced growth, disease resistance and insect resistance to plants,  
PT especially vegetables and ornamental flowers.  
XX  
PS Disclosure; Page 12-13; 100pp; English.  
XX  
XX The present sequence represents a hypersensitive response elicitor  
CC polypeptide. The specification describes hypersensitive response elicitor  
CC polypeptide fragments, which do not elicit a hypersensitive response.  
CC Instead, the proteins impart disease resistance to plants, enhance plant  
CC growth, and/or control insects. The polypeptide fragments may be used to  
CC these properties to plants. The plants which may be treated in this way  
CC include vegetables, crops and ornamental plants such as alfalfa, rice,  
CC wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet  
CC potato, bean, pea, chickory, lettuce, endive, cabbage, brussel sprout,  
CC beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion,  
CC garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini,  
CC cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry,  
CC pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis  
CC thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum,  
CC carnation or zinnia  
XX  
SQ Sequence 447 AA;  
Query Match 100.0%; Score 2310; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSILTLNNNTSSPGLFQSGGNGLGHNANSALGQOPIDRTIQEOMALLAELLKSLLS 60  
DB 1 MSILTLNNNTSSPGLFQSGGNGLGHNANSALGQOPIDRTIQEOMALLAELLKSLLS 60  
QY 61 POSGNAATGAGNDQITGVNAGGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
DB 61 POSGNAATGAGNDQITGVNAGGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
QY 121 QGGGQIGDNPLKAMLKLIARMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
DB 121 QGGGQIGDNPLKAMLKLIARMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
QY 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDFFSSPTKAAAGGSTPVTDHPDVGSAIGAG 240  
DB 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDFFSSPTKAAAGGSTPVTDHPDVGSAIGAG 240  
QY 241 NSVAFTSAGANQTVLHDTITTVKAGQVFDGKGTFTAGSELGQGGQSENOKPLFILEDGS 300  
DB 241 NSVAFTSAGANQTVLHDTITTVKAGQVFDGKGTFTAGSELGQGGQSENOKPLFILEDGS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSKSHVEITNSSFEHSD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSKSHVEITNSSFEHSD 360  
QY 361 KILQLNADTNLSVDNVKAKDFGTFVRTNGGQQGNWDLNLSHISAEDKFSFVKSDSEGLN 420  
DB 361 KILQLNADTNLSVDNVKAKDFGTFVRTNGGQQGNWDLNLSHISAEDKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
RESULT 4  
AA022548  
ID AAO22548 standard; protein; 447 AA.  
XX  
AC AAO22548;  
XX  
XX 28-OCT-2002 (first entry)  
XX  
XX Hypersensitive response elicitor protein #2 from Erwinia amylovora.  
XX

KW Desiccation inhibitor; longevity enhancer; desiccation inhibitor;  
KW cutting; ornamental plant; hypersensitive response elicitor protein;  
KW transgenic ornamental plant; early flowering; longevity enhancer; plant;  
XX flower bloom; flower.  
XX  
OS Erwinia amylovora.  
XX  
PN WO200237960-A2.  
XX  
PD 16-MAY-2002.  
XX  
XX 06-NOV-2001; 2001WO-US043715.  
XX  
XX 13-NOV-2000; 2000US-0248169P.  
XX  
XX (EDEN-) EDEN BIOSCIENCE CORP.  
XX  
XX Wei Z, Leon E, Oviedo A;  
XX  
XX WPI; 2002-575194/61.  
XX  
XX N-PSDB; AAL41133.  
XX  
XX Inhibiting desiccation of cuttings from ornamental plants, by treating  
PT ornamental plants with hypersensitive response elicitor protein, or  
PT expressing heterologous hypersensitive response elicitor protein in  
PT plants.  
XX  
XX Disclosure; Page 12-13; 69pp; English.  
XX  
XX The invention relates to a method for inhibiting desiccation of cuttings  
CC from ornamental plants. The method involves treating the cuttings with a  
CC hypersensitive response elicitor protein or polypeptide, or providing a  
CC transgenic ornamental plant or plant seed transformed with a DNA molecule  
CC encoding the hypersensitive response elicitor polypeptide, and growing  
CC the ornamental plant or transgenic ornamental plant produced from the  
CC transgenic ornamental plant seed. The hypersensitive response elicitor  
CC protein or polypeptide is useful for inhibiting desiccation of cuttings  
CC from ornamental plants, for harvesting cuttings from ornamental plants,  
CC for promoting early flowering of ornamental plants, and enhancing the  
CC longevity of flower blooms on ornamental plant cuttings. This sequence  
CC represents a hypersensitive response elicitor protein of the invention  
XX  
SQ Sequence 447 AA;  
Query Match 100.0%; Score 2310; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSILTLNNNTSSPGLFQSGGNGLGHNANSALGQOPIDRTIQEOMALLAELLKSLLS 60  
DB 1 MSILTLNNNTSSPGLFQSGGNGLGHNANSALGQOPIDRTIQEOMALLAELLKSLLS 60  
QY 61 POSGNAATGAGNDQITGVNAGGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
DB 61 POSGNAATGAGNDQITGVNAGGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
QY 121 QGGGQIGDNPLKAMLKLIARMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
DB 121 QGGGQIGDNPLKAMLKLIARMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
QY 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDFFSSPTKAAAGGSTPVTDHPDVGSAIGAG 240  
DB 181 PSGNSPSGNYSPVSTFSPSTPTSPSLDFFSSPTKAAAGGSTPVTDHPDVGSAIGAG 240  
QY 241 NSVAFTSAGANQTVLHDTITTVKAGQVFDGKGTFTAGSELGQGGQSENOKPLFILEDGS 300  
DB 241 NSVAFTSAGANQTVLHDTITTVKAGQVFDGKGTFTAGSELGQGGQSENOKPLFILEDGS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSKSHVEITNSSFEHSD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSKSHVEITNSSFEHSD 360  
QY 361 KILQLNADTNLSVDNVKAKDFGTFVRTNGGQQGNWDLNLSHISAEDKFSFVKSDSEGLN 420  
DB 361 KILQLNADTNLSVDNVKAKDFGTFVRTNGGQQGNWDLNLSHISAEDKFSFVKSDSEGLN 420

```

Db      361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
QY      421 VNTSDISLGDVENHYKVPMSANLKVAE 447
Db      421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 5
AAE18296
ID AAE18296 standard; protein; 447 AA.
XX
AC AAE18296;
DT
DT 07-MAY-2002 (first entry)
XX
DE Erwinia amylovora hypersensitive response elicitor (HRE) #2.
XX
KW Hypersensitive response elicitor; HRE; transgenic plant; plant growth;
KW stress tolerance; disease tolerance; modified flower colour;
KW insect resistance; herbicide resistance; male sterility.
XX
OS Erwinia amylovora.
XX
PN WO200195724-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US018955.
XX
PR 15-JUN-2000; 2000US-0211585P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Derocher J;
XX
DR WPI; 2002-130707/17.
XX
DR N-PSDB; AAD29125.
XX
PT Improving effectiveness of transgenic plants by topical application of a
PT hypersensitive response elicitor protein to the transgenic plant or by
PT incorporating into the plant a transgene encoding the protein.
XX
PS Disclosure; Page 13-14; 86pp; English.
XX
CC The invention relates to methods of improving the effectiveness of
CC transgenic plants which involves either topical application of a
CC hypersensitive response elicitor (HRE) protein to the transgenic plant or
CC incorporating into the transgenic plant a transgene encoding HRE. HRE
CC sequence is used for improving the effectiveness of transgenic plants by
CC maximising the benefit of transgenic traits associated with a deleterious
CC effect on growth, stress tolerance, disease or insect resistance.
CC enhanced growth, herbicide resistance, male sterility, modified flower
CC colour and biochemically modified plant product in the transgenic plants
CC or overcoming the deleterious effects. The present sequence is Erwinia
CC amylovora HRE protein
XX
SQ Sequence 447 AA;

Query Match      100.0%; Score 2310; DB 5; Length 447;
Best Local Similarity 100.0%; Pred. NO. 2.4e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSILTIANNNTSSPGLFQSGGDNGLGHNANSALGQOPIDROTIEQMAQLLAELKSLLS 60
Db      1 MSILTIANNNTSSPGLFQSGGDNGLGHNANSALGQOPIDROTIEQMAQLLAELKSLLS 60
QY      61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTPQSDSQNMLSEMGNGLDQAITPDG 120
Db      61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTPQSDSQNMLSEMGNGLDQAITPDG 120
QY      121 QGGGQIGDNPLLKAMLKLIARMDGQSDQFGQPGTGNNNSASGTSSSGSPNDLSGGKA 180

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Db      121 QGGGQIGDNPLLKAMLKLIARMDGQSDQFGQPGTGNNNSASGTSSSGSPNDLSGGKA 180
QY      181 PSGNSPSGNYSPVSTFSPSTPTSPDLPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
Db      181 PSGNSPSGNYSPVSTFSPSTPTSPDLPSSPTKAAGGSTPVTDHPDPVGSAGIGAG 240
QY      241 NSVAFTSAGANQTVLHDITITVKAGQVFDGKQGTFTAGSELGDDGQSENQKPLFILEDGAS 300
Db      241 NSVAFTSAGANQTVLHDITITVKAGQVFDGKQGTFTAGSELGDDGQSENQKPLFILEDGAS 300
QY      301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGEDAITVKPNSAGKSKSHVEITNSSFEHSD 360
Db      301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGEDAITVKPNSAGKSKSHVEITNSSFEHSD 360
QY      361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
Db      361 KILQNLADTNLSVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN 420
QY      421 VNTSDISLGDVENHYKVPMSANLKVAE 447
Db      421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 6
AAE16448
ID AAE16448 standard; protein; 447 AA.
XX
AC AAE16448;
DT
DT 09-APR-2002 (first entry)
XX
DE E. amylovora hypersensitive response elicitor protein #2.
XX
KW Hypersensitive response elicitor protein; plant growth; fruit coloration;
KW disease resistance; stress resistance; phytotoxin; insect infection;
KW plant maturation.
XX
OS Erwinia amylovora.
XX
FH Key Location/Qualifiers
FT Domain 5..64 /label= Hypersensitive_response_eliciting_domain_1
FT Region 5..45 /label= Acidic_unit
FT Region 45..64 /label= Alpha_helix
FT Domain 103..146 /label= Hypersensitive_response_eliciting_domain_2
FT Region 103..131 /label= Acidic_unit
FT Region 131..146 /label= Alpha_helix
XX
PN WO200198501-A2.
XX
PD 27-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US018820.
XX
PR 16-JUN-2000; 2000US-0212211P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Fan H, Wei Z;
XX
DR WPI; 2002-122282/16.
XX
DR N-PSDB; AAD27016.
XX
New hypersensitive response elicitor proteins comprising spaced apart
PT domains having an acidic portion linked to an alpha-helix, useful for
PT imparting disease or stress resistance, controlling insects or enhancing
PT plant growth.
XX

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PS Disclosure; Page 13-14; 99pp; English.

XX The patent discloses hypersensitive response elicitor proteins and nucleotides encoding such proteins. Hypersensitive response elicitor proteins comprise an isolated pair or more of spaced apart domains, each comprising an acidic portion linked to an alpha-helix and capable of eliciting a hypersensitive response in plants. Sequences of the invention are used to impart disease resistance to plants, to enhance plant growth, to control insects and/or to impart stress resistance to plants which include resistance to environmental stresses such as climate, air pollution, chemical and nutritional stress. The method of imparting disease resistance has the potential for treating previously untreatable diseases, treating diseases systemically and avoiding the use of infectious agents or environmentally harmful materials. Hyper- sensitive response elicitor sequences are used to enhance plant growth which encompasses greater yield, increased in quantity of seeds produced, percentage of seeds germinated, plant size and biomass, bigger fruits, earlier fruit coloration and plant maturation. They are also used for insect control which encompasses preventing direct insect damage to plant by feeding injury, interfering with insect larval feeding on the plants, preventing insects from colonising host plants and releasing phytotoxins. Sequences of the invention also prevent subsequent disease damage to plants resulting from insect infection. The present sequence is Erwinia amylovora hypersensitive response elicitor protein

XX Sequence 447 AA;

Query Match 100.0%; Score 2310; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGDNGLGCHNANSALGQOPIDRTQIEQMAQLLELLKSLLS 60  
DB 1 MSILTLNNNTSSPGLFQSGDNGLGCHNANSALGQOPIDRTQIEQMAQLLELLKSLLS 60

QY 61 POSGNAATGAGNDQTTGVNAGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
DB 61 POSGNAATGAGNDQTTGVNAGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120

QY 121 QGGGQIGDNPLLKAMLKLIARMDGSDQFGPGTGNNSSASGTSSSGGSPFNDLSGGKA 180  
DB 121 QGGGQIGDNPLLKAMLKLIARMDGSDQFGPGTGNNSSASGTSSSGGSPFNDLSGGKA 180

QY 181 PSGNPSGNYSPVSTFSPSTPTSPPLDFFSSPTKAAAGGTPVTDHPDVGSAIGAG 240  
DB 181 PSGNPSGNYSPVSTFSPSTPTSPPLDFFSSPTKAAAGGTPVTDHPDVGSAIGAG 240

QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGGQSENOKPLFILEDGS 300  
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGGQSENOKPLFILEDGS 300

QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 7  
ABB09226  
ID ABB09226 standard; protein; 447 AA.  
XX  
AC ABB09226;  
XX  
DT 08-JUL-2002 (first entry)  
XX  
DE Erwinia amylovora hypersensitive response elicitor SEQ ID NO:5.

XX Hypersensitive response elicitor; fruit; vegetable; plant; desiccation; postharvest disease.  
KW Erwinia amylovora.  
OS WO200180639-A2.  
PN 01-NOV-2001.  
PD 17-APR-2001; 2001WO-US012468.  
PF 19-APR-2000; 2000US-0198359P.  
PR (EDEN-) EDEN BIOSCIENCE CORP.  
PA Wei Z, Qiu D, Remick D;  
PI WPI: 2002-041357/05.  
XX N-PSDB; ABL51711.  
XX Inhibiting post harvest disease (caused by Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and enhancing the longevity in a fruits or vegetables, using hypersensitive response elicitor proteins or nucleic acids.  
XX Disclosure; Page 11-12; 72pp; English.  
XX The present invention describes methods for inhibiting post harvest disease or desiccation and enhancing the longevity in a fruits or vegetables, using hypersensitive response elicitor proteins or polypeptides or nucleic acids (I) derived from pathogens (e.g. Erwinia amylovora, E. stewartii, E. chrysanthemi, E. carotovora, Xanthomonas, Pseudomonas syringae, P. solanacearum, Phytophthora, and Clavibacter). (I) has bactericidal activity, and can be used in gene therapy. The method can be used for inhibiting post harvest disease (caused by Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and enhancing the longevity in a fruits or vegetables. The method enables growers, warehouse packers, shippers and suppliers to process, handle and store fruit and vegetables with reduced losses caused by post harvest disease and desiccation, therefore reducing costs to the consumer and improving quality. The present sequence represents a hypersensitive response elicitor protein given in the exemplification of the present invention

XX Sequence 447 AA;

Query Match 100.0%; Score 2310; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGDNGLGCHNANSALGQOPIDRTQIEQMAQLLELLKSLLS 60  
DB 1 MSILTLNNNTSSPGLFQSGDNGLGCHNANSALGQOPIDRTQIEQMAQLLELLKSLLS 60

QY 61 POSGNAATGAGNDQTTGVNAGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120  
DB 61 POSGNAATGAGNDQTTGVNAGLNGRGTAGTTTQSDSQNMLSEMGNGLDQAITPDG 120

QY 121 QGGGQIGDNPLLKAMLKLIARMDGSDQFGPGTGNNSSASGTSSSGGSPFNDLSGGKA 180  
DB 121 QGGGQIGDNPLLKAMLKLIARMDGSDQFGPGTGNNSSASGTSSSGGSPFNDLSGGKA 180

QY 181 PSGNPSGNYSPVSTFSPSTPTSPPLDFFSSPTKAAAGGTPVTDHPDVGSAIGAG 240  
DB 181 PSGNPSGNYSPVSTFSPSTPTSPPLDFFSSPTKAAAGGTPVTDHPDVGSAIGAG 240

QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGGQSENOKPLFILEDGS 300  
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGGQSENOKPLFILEDGS 300

QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSHVITNSSFHASD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSHVITNSSFHASD 360

QY 361 KILQLNADTNLSVDNVKADFGFTVTNGGQQGNWDNLNLSHAEDKFSFVKSDSEGLN 420  
DB 361 KILQLNADTNLSVDNVKADFGFTVTNGGQQGNWDNLNLSHAEDKFSFVKSDSEGLN 420

QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447



```
CC stress resistance to plants
XX Sequence 424 AA;
SQ
  Query Match      24.2%; Score 559; DB 3; Length 424;
  Best Local Similarity 36.1%; Pred. No. 2.7e-30;
  Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;

QY 37 QPIDRQTIEQMAQLLAELKSL----LSPOSQNAATGAGGNDQTTGVGNAGGLNGRKGATG 93
Db 72 KENDSQS--NIAKLISALIMSLLOMLTNSNKKQDTNQEQDPSQAPFQNNGLG-----122

QY 94 TTPQSDSQNMLSEMGNGLDQAITPDGCGGQIGDNPPLKMLKLIARMMDGSDQFGQP 153
Db 123 -TPSADS-----GGGG-----TPDATGGGG-GDTP-----SATGGG 151

QY 154 GTGNNSASGTSSSGSGSPFNDLSGKAPSGNSPVSPTSPTSPLDFFS 213
Db 152 GDDTPTATGGGSGGGTPTATGGG---SGGTPATGGGEGGVTPOITPQL-----A 200

QY 214 SPTKAAGGSTPVDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDITTVKAGQVDFGKGT 273
Db 246 FTADKSMGNDQGENQKPMFELAEAGATLKNVNLGENEVDGIHVAKNAQAEVTDINVHAQN 305

QY 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKILOLNADTNLSVDNVKAKDGTFTVRTNG 389
Db 306 VGEDLITVKGEGGAATVNLINIKNSAKGADDKVQVQLNANTHLKIDNFKADDFGTWRTNG 365

QY 390 GQO-GNWDNLNLHISAEDGKFSFKVSDSEGLNVNTSDISLGDVENHY 435
Db 366 GKQFDDMSIELNGIEANHGKFAVKSDSDDLKATGNIAMTDVKHAY 412

RESULT 10
AA022550
ID AA022550 standard; protein; 424 AA.
XX
AC AA022550;
XX
DT 08-AUG-2000 (first entry)
DE A hypersensitive response elicitor protein.
XX
KW Hypersensitive response; insect control; disease resistance;
KW hypersensitive response elicitor; plant growth; vegetable; crop;
KW ornamental plant.
XX
OS Pseudomonas syringae.
XX
PN WO200020452-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023181.
XX
PR 05-OCT-1998; 98US-0103050P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Fan H, Niggemeyer JL;
XX
DR WPI; 2000-303745/26.
XX
DR N-PSDB; AAA14943.
XX
PT Hypersensitive response elicitor polypeptides useful for imparting
PT enhanced growth, disease resistance and insect resistance to plants,
PT especially vegetables and ornamental flowers.
XX
PS Disclosure; Page 26-28; 100pp; English.
```

```
XX The present sequence represents a hypersensitive response elicitor
CC polypeptide. The specification describes hypersensitive response elicitor
CC polypeptide fragments, which do not elicit a hypersensitive response.
CC Instead, the proteins impart disease resistance to plants, enhance plant
CC growth, and/or control insects. The polypeptide fragments may be used to
CC these properties to plants. The plants which may be treated in this way
CC include vegetables, crops and ornamental plants such as alfalfa, rice,
CC wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet
CC potato, bean, pea, chickory, lettuce, endive, cabbage, brussel sprout,
CC beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion,
CC garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini,
CC cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry,
CC pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis
CC thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum,
CC carnation or zinnia
XX
SQ Sequence 424 AA;
  Query Match      24.2%; Score 559; DB 3; Length 424;
  Best Local Similarity 36.1%; Pred. No. 2.7e-30;
  Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;

QY 37 QPIDRQTIEQMAQLLAELKSL----LSPOSQNAATGAGGNDQTTGVGNAGGLNGRKGATG 93
Db 72 KENDSQS--NIAKLISALIMSLLOMLTNSNKKQDTNQEQDPSQAPFQNNGLG-----122

QY 94 TTPQSDSQNMLSEMGNGLDQAITPDGCGGQIGDNPPLKMLKLIARMMDGSDQFGQP 153
Db 123 -TPSADS-----GGGG-----TPDATGGGG-GDTP-----SATGGG 151

QY 154 GTGNNSASGTSSSGSGSPFNDLSGKAPSGNSPVSPTSPTSPLDFFS 213
Db 152 GDDTPTATGGGSGGGTPTATGGG---SGGTPATGGGEGGVTPOITPQL-----A 200

QY 214 SPTKAAGGSTPVDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDITTVKAGQVDFGKGT 273
Db 201 NPNRTSG-----TGSVSDTAGS---TEQAGKINVVKDTIKVGAGEVDFGHGAT 245

QY 274 FTAGSELGDSQENOKPLFILEDGASLKNVTMGDDGADGIHLYG---DAKIDNLHVNT 329
Db 246 FTADKSMGNDQGENQKPMFELAEAGATLKNVNLGENEVDGIHVAKNAQAEVTDINVHAQN 305

QY 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKILOLNADTNLSVDNVKAKDGTFTVRTNG 389
Db 306 VGEDLITVKGEGGAATVNLINIKNSAKGADDKVQVQLNANTHLKIDNFKADDFGTWRTNG 365

QY 390 GQO-GNWDNLNLHISAEDGKFSFKVSDSEGLNVNTSDISLGDVENHY 435
Db 366 GKQFDDMSIELNGIEANHGKFAVKSDSDDLKATGNIAMTDVKHAY 412

RESULT 11
AA022550
ID AA022550 standard; protein; 424 AA.
XX
AC AA022550;
XX
DT 28-OCT-2002 (first entry)
DE Hypersensitive response elicitor protein #2 from Pseudomonas syringae.
XX
KW Desiccation inhibitor; longevity enhancer; desiccation inhibitor;
KW cutting; ornamental plant; hypersensitive response elicitor protein;
KW transgenic ornamental plant; early flowering; longevity enhancer; plant;
KW flower bloom; flower.
XX
OS Pseudomonas syringae.
XX
PN WO200237960-A2.
XX
PD 16-MAY-2002.
XX
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PF 06-NOV-2001; 2001WO-US043715.
XX
PR 13-NOV-2000; 2000US-0248169P.
XX
XX (EDEN-) EDEN BIOSCIENCE CORP.
PA
XX Wei Z, Leon E, Oviedo A;
XX
XX WPI: 2002-575194/61.
DR
DR N-PSDB; AAL41135.
XX
XX Inhibiting desiccation of cuttings from ornamental plants, by treating
PT ornamental plants with hypersensitive response elicitor protein, or
PT expressing heterologous hypersensitive response elicitor protein in
PT plants.
XX
XX Disclosure; Page 16-17; 69pp; English.
XX
XX The invention relates to a method for inhibiting desiccation of cuttings
CC from ornamental plants. The method involves treating the cuttings with a
CC hypersensitive response elicitor protein or polypeptide, or providing a
CC transgenic ornamental plant or plant seed transformed with a DNA molecule
CC encoding the hypersensitive response elicitor polypeptide, and growing
CC the ornamental plant or transgenic ornamental plant produced from the
CC transgenic ornamental plant seed. The hypersensitive response elicitor
CC protein or polypeptide is useful for inhibiting desiccation of cuttings
CC from ornamental plants, for harvesting cuttings from ornamental plants,
CC for promoting early flowering of ornamental plants, and enhancing the
CC longevity of flower blooms on ornamental plant cuttings. This sequence
CC represents a hypersensitive response elicitor protein of the invention
XX
XX Sequence 424 AA;
SQ
Query Match 24.2%; Score 559; DB 5; Length 424;
Best Local Similarity 36.1%; Pred. No. 2.7e-30;
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;
QY 37 QPIDRTIQMAQLLAELLKSL---LSPQSGNAATGAGGNDQTTGVNAGGLNGRKGATAG 93
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
72 KPNDSSQ--NIAKLISALIMSLLOMLTNSNKKQDTNQEOPDSQAPFQNNGLG----- 122
QY 94 TTPQSDSQNMLSEMNGNLDQAITPDGQGGQIGDNPLLKAMLKLIARMWDQSDFGQP 153
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 -TPSADS-----GGGG-----TPDATGGGG-GDTP-----SATGGG 151
QY 154 GTGNNSASGTSSSGGSPFNDLSGGKAPSGNSPGNSPVSTFSPSTPTSPSLDRPS 213
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 GGDPTATGGGGGGGGTPTATGGG---SGGTPATGGGGGVTQIITPOL-----A 200
QY 214 SPTKAAGGSTPTVTHDPDVGSGAGIAGNSVAFTSAGANQTVLHDTITVKAGQVFDKGQT 273
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201 NPNRTSG-----TGSVSDTAGS---TEQAGKINVVKDTIKVGAGEVFDGHGAT 245
QY 274 FTAGSELGGGQSENGKPLFILEDGASLKNVTMGDDGADGIHLYG-----DAKIDNLHVTN 329
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
246 FTADKSMGNGDQENQKPFELAEAGATLKNVNLGENEVDGIHVAKNAQAEVTDINVAHQN 305
QY 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKILOLNADTNLSVDNVKAKDFGTFVRTNG 389
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VGEDLITVKGEGGAATVNLINIKNSAKGADDKVVQLNANTHLKIDNFRADDFGTVRTNG 365
QY 390 GQO-GNWDNLNLSHISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHY 435
366 GKQFDDMSIELNGIEANHGKFAIVKSDSDDLKATGNTIAMTVDVGHAY 412

```

RESULT 12  
 AAE18298  
 ID AAE18298 standard; protein; 424 AA.  
 XX  
 AC AAE18298;  
 XX  
 DT 07-MAY-2002 (first entry)

Pseudomonas syringae hypersensitive response elicitor (HRE) #2.  
 Hypersensitive response elicitor; HRE; transgenic plant; plant growth;  
 stress tolerance; disease tolerance; modified flower colour;  
 insect resistance; herbicide resistance; male sterility.  
 Pseudomonas syringae.  
 WO200195724-A2.  
 20-DEC-2001.  
 13-JUN-2001; 2001WO-US018955.  
 15-JUN-2000; 2000US-0211585P.  
 (EDEN-) EDEN BIOSCIENCE CORP.  
 Wei Z, Derocher J;  
 WPI: 2002-130707/17.  
 N-PSDB; AAD29127.  
 Improving effectiveness of transgenic plants by topical application of a  
 hypersensitive response elicitor protein to the transgenic plant or by  
 incorporating into the plant a transgene encoding the protein.  
 Disclosure; Page 17-18; 86pp; English.  
 The invention relates to methods of improving the effectiveness of  
 transgenic plants which involves either topical application of a  
 hypersensitive response elicitor (HRE) protein to the transgenic plant or  
 incorporating into the transgenic plant a transgene encoding HRE. HRE  
 sequence is used for improving the effectiveness of transgenic plants by  
 maximising the benefit of transgenic traits associated with a deleterious  
 effect on growth, stress tolerance, disease or insect resistance,  
 enhanced growth, herbicide resistance, male sterility, modified flower  
 colour and biochemically modified plant product in the transgenic plants  
 or overcoming the deleterious effects. The present sequence is  
 Pseudomonas syringae HRE protein

366 GKQFDDMSIELNGIEANHGKFAVKSDDDLKLTATGNIAMTDVKHAY 412

RESULT 13

AAE16452

ID AAE16452 standard; protein; 424 AA.

AC AAE16452;

DT 09-APR-2002 (first entry)

DE P. syringae hypersensitive response elicitor protein, dspe.

KW Hypersensitive response elicitor protein; plant growth; fruit coloration; disease resistance; stress resistance; phytotoxin; insect infection; plant maturation; dspe protein.

OS Pseudomonas syringae.

FH Key Location/Qualifiers

FT Domain 45..102

FT /label= Hypersensitive\_response\_eliciting\_domain

FT Region 45..79

FT /label= Acidic\_unit

FT Region 79..102

FT /label= Alpha\_helix

XX WO200198501-A2.

XX 27-DEC-2001.

XX 12-JUN-2001; 2001WO-US018820.

XX 16-JUN-2000; 2000US-021211P.

XX (EDEN-) EDEN BIOSCIENCE CORP.

XX Fan H, Wei Z;

XX WPI: 2002-122282/16.

XX N-PSDB; AAD27020.

XX New hypersensitive response elicitor proteins comprising spaced apart domains having an acidic portion linked to an alpha-helix, useful for imparting disease or stress resistance, controlling insects or enhancing plant growth.

XX Disclosure; Page 28-29; 99pp; English.

XX The patent discloses hypersensitive response elicitor proteins and nucleotides encoding such proteins. Hypersensitive response elicitor proteins comprise an isolated pair or more of spaced apart domains, each comprising an acidic portion linked to an alpha-helix and capable of eliciting a hypersensitive response in plants. Sequences of the invention are used to impart disease resistance to plants, to enhance plant growth, to control insects and/or to impart stress resistance to plants which includes resistance to environmental stresses such as climate, air pollution, chemical and nutritional stress. The method of imparting disease resistance has the potential for treating previously untreatable diseases, treating diseases systemically and avoiding the use of infectious agents or environmentally harmful materials. Hyper-sensitive response elicitor sequences are used to enhance plant growth which encompasses greater yield, increased in quantity of seeds produced, percentage of seeds germinated, plant size and biomass, bigger fruits, earlier fruit coloration and plant maturation. They are also used for insect control which encompasses preventing direct insect damage to plant by feeding injury, interfering with insect larval feeding on the plants, preventing insects from colonising host plants and releasing phytotoxins. Sequences of the invention also prevent subsequent disease damage to plants resulting from insect infection. The present sequence is Pseudomonas syringae hypersensitive response elicitor protein, dspe

SQ Sequence 424 AA;

Query Match 24.2%; Score 559; DB 5; Length 424;  
Best Local Similarity 36.1%; Pred. No. 2.7e-30;  
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;

QY 37 QPIDRQTTEOMAQLLAELKSL---LSPOSNAATGAGGNDQTTGVGNAGGLNGRGTAG 93  
DB 72 KENDSQS--NIAKLIISALIMSLLOMLTNSNKKQDTNQEOPDSQAPFQNNGLG----- 122

QY 94 TTPQSDSQNMLSEMGNGNGLDQAITPDGCGGQIGDNPLLKMLKLIARWMDGSDQFGOP 153  
DB 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151

QY 154 GTGNNSASGTSSSGSPFNLSGGKAPSGNSGNYSPVSTFSPSTPTSPPLDPPS 213  
DB 152 GGDTPATGCGGGGGGTPTATGGG---SGGTPTATGGGEGGVTPTITPOL-----A 200

QY 214 SPTKAAGSTPVTDPDPVGSAGIGAGNSVATISAGANQTVLHDTITVKAQGVDFGKGT 273  
DB 201 NPNRTSG-----TGSVSDTAGS---TEQAGKINVVKDTIKVGAGEYFDGHGAT 245

QY 274 FTAGSELGPGGSENGKPLFILEDGASLKNVTMGDDGADGHIHYG---DAKIDNLHVTN 329  
DB 246 FTADKSMGNGDQENKQKPFELAEAGATLKNVLGENEVDGIHVAKNAQEVITIDNVHAQN 305

QY 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFTVRTNG 389  
DB 306 VGEDLITVKGEGAAVTNLNKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTWVRTNG 365

QY 390 GQQ-GNWDNLNLSHISAEDKGFVKSDEGLNVNTSDISLGDEVNHY 435

DB 366 GKQFDDMSIELNGIEANHGKFAVKSDDDLKLTATGNIAMTDVKHAY 412

RESULT 14

ABB09228

ID ABB09228 standard; protein; 424 AA.

AC ABB09228;

DT 08-JUL-2002 (first entry)

DE P. syringae hypersensitive response elicitor protein SEQ ID NO:9.

XX Hypersensitive response elicitor; fruit; vegetable; plant; desiccation; postharvest disease.

OS Pseudomonas syringae.

XX WO200180639-A2.

XX 01-NOV-2001.

XX 17-APR-2001; 2001WO-US012468.

XX 19-APR-2000; 2000US-0198359P.

XX (EDEN-) EDEN BIOSCIENCE CORP.

XX Wei Z, Qiu D, Remick D;

XX WPI: 2002-041357/05.

XX N-PSDB; ABL51713.

XX Inhibiting post harvest disease (caused by Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and enhancing the longevity in a fruits or vegetables, using hypersensitive response elicitor proteins or nucleic acids.

XX Disclosure; Page 15-16; 72pp; English.

XX The present invention describes methods for inhibiting post harvest

CC disease or desiccation and enhancing the longevity in a fruits or  
CC vegetables, using hypersensitive response elicitor proteins or  
CC polypeptides or nucleic acids (I) derived from pathogens (e.g. Erwinia  
CC amylovora, E. stewartii, E. chrysanthemi, E. carotovora, Xanthomonas,  
CC Pseudomonas syringae, P. solanacearum, Phytophthora, and Clavibacter).  
CC (I) has bactericidal activity, and can be used in gene therapy. The  
CC method can be used for inhibiting post harvest disease (caused by  
CC Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and  
CC enhancing the longevity in a fruits or vegetables. The method enables  
CC growers, warehouse packers, shippers and suppliers to process, handle and  
CC store fruit and vegetables with reduced losses caused by post harvest  
CC disease and desiccation, therefore reducing costs to the consumer and  
CC improving quality. The present sequence represents a hypersensitive  
CC response elicitor protein given in the exemplification of the present  
CC invention  
XX  
SQ Sequence 424 AA;

Query Match 24.2%; Score 559; DB 5; Length 424;  
Best Local Similarity 36.1%; Pred. No. 2.7e-30;  
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;  
QY 37 QPIDQTIQMAQLLAELIKSL---LSPOSNAATGAGNDQTTGVGNAGLNGRKGTAG 93  
DB 72 KPNDSSQS--NIAKLIASALIMSLQMLTNSNKKQDTNQEQPDSQAPPQNNGLG----- 122  
QY 94 TTPQSDSQNMLSEMGNGLDQAITPDGQGGQIGDNPPLKAMKLIARMMDGQSDQFGQP 153  
DB 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151  
QY 154 GTGNNSASGTSSSGGSPPNDLSGGKAPSGNSPVSPTSPSTPTSPPLDPPS 213  
DB 152 GGDTPATCGGSGGGGCTPTATGGG---SGGTPATGGGEGGVTPOITPQL-----A 200  
QY 214 SPTKAAGSTPTDHPDPVGSAGIAGNSVATSAGANTVLHDTITVKAGVFDGKGOT 273  
DB 201 NPNRTSG-----TGVSVDSTAGS-----TEQAGKINNVKDTIKVGAQVFDGHGAT 245  
QY 274 FTAGSELGDSQSENOKPLFILEDGASLKNVTMGDDGADGHIHYG-----DAKIDNLHVTN 329  
DB 246 FTADKSMGNGDQENQKPFELAEAGTAKNVLGENEVDGIHVAKNAQEVTDINVAQN 305  
QY 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKILOLNADTNLSVDNVKAKDFGTFTVNTG 389  
DB 306 VGEDLITVKEGGAAVTNLNINSSAKGADDKVVQLNANTHLKIDNFKADDFGTMTVRTG 365  
QY 390 GOQ-GNWDNLNLSHISEDGKFSFKSDSEGLNVNTSDISLGDVENHY 435  
DB 366 GKQFDMSIELNGIEANHGKFALVKSDSDDLKATGNIAMTQVKHAY 412

RESULT 15  
AAW83014  
ID AAW83014 standard; protein; 197 AA.  
XX  
AC AAW83014;  
XX  
DT 28-JAN-1999 (first entry)  
XX  
XX Bacillus sp strain KSM-PI5 pectic acid lyase.  
DE  
XX Bacillus sp.  
XX  
XX WO9845393-A2.  
XX  
XX 15-OCT-1998.  
XX  
XX 08-APR-1998; 98WO-JP001613.  
XX

PR 09-APR-1997; 97JP-00091142.  
PR 08-SEP-1997; 97JP-00242736.  
XX  
PA (KAOS ) KAO CORP.  
XX  
PI Wada Y, Kasai M, Shikata S, Suzumatsu A, Koike K, Hatada Y;  
PI Kobayashi T, Ito S, Tsumadori M;  
XX  
WI 1998-568339/48.  
DR N-PSDB; AAV69879.  
XX  
XX Detergent composition containing protopectinase active at alkaline pH -  
PT on protopectin and polygalacturonic acid, provides better removal of  
PT muddy soil.  
XX  
PS Example; Page 71-72; 80pp; English.  
XX  
CC The present invention describes a detergent composition which contains a  
CC protopectinase having an optimum pH 7 or higher against protopectin and  
CC polygalacturonic acid substrates. Inclusion of protopectinase gives a  
CC composition that provides better removal of muddy soil, particularly from  
CC socks. The present sequence represents pectic acid lyase from Bacillus  
CC sp. strain KSM-PI5, which is used in an example from the present  
CC invention. Pectic acid lyase exhibits protopectinase activity  
XX  
SQ Sequence 197 AA;  
Query Match 15.6%; Score 359.5; DB 2; Length 197;  
Best Local Similarity 46.3%; Pred. No. 6.2e-17;  
Matches 81; Conservative 29; Mismatches 56; Indels 9; Gaps 4;  
QY 253 TVLHDTITVKAGQVFDGKGOTFTAG-SELGDSQSENOKPLFILEDGASLKNVTMGDDGA 311  
DB 3 TVVHETIRVPAQTFDGGQTVVNPNTLGDGSAENQKPIFRLGAGASLKNVWIGAPAA 62  
QY 312 DGIHLYGDAKIDNLHVTNVEDAITVKPNSAGKSHVEITNSSFEHASDKILOLNADTNL 371  
DB 63 DGVHCYGDCTITNVIWEDVGEDALTK--SSGT---VNISGAAYKAYDKVFQINAAGTI 117  
QY 372 SVDNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFKSDSE---GLNVNT 423  
DB 118 NIRNFRADDIGKLVQRQNGTGYKVMNVNENCNISRVKDAILRTDSSTSTGRIVNT 172  
Search completed: January 25, 2005, 16:05:58  
Job time : 160 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 15:53:21 ; Search time 40 Seconds  
(without alignments)  
741.104 Million cell updates/sec

Title: US-09-879-248-6  
Perfect score: 2310  
Sequence: 1 MSILTLNNTSSPGLFQSG.....LGDVENHYKVPMSANLKVAE 447

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCUS COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2310	100.0	447	3 US-09-120-927-2	Sequence 2, Appli
2	2310	100.0	447	4 US-09-431-614-6	Sequence 6, Appli
3	559	24.2	424	3 US-09-120-817-2	Sequence 2, Appli
4	559	24.2	424	4 US-09-431-614-14	Sequence 14, Appli
5	359.5	15.6	197	3 US-09-402-668-2	Sequence 2, Appli
6	341	14.8	221	3 US-09-198-956-4	Sequence 4, Appli
7	341	14.8	221	4 US-09-670-141-4	Sequence 4, Appli
8	190.5	8.2	62	3 US-09-402-668-10	Sequence 10, Appli
9	181.5	7.9	2411	3 US-09-268-347-36	Sequence 36, Appli
10	174	7.5	2042	4 US-09-077-098A-6	Sequence 6, Appli
11	165.5	7.2	344	1 US-08-891-254-7	Sequence 7, Appli
12	165.5	7.2	344	2 US-08-819-539-7	Sequence 7, Appli
13	165.5	7.2	344	3 US-09-030-270A-7	Sequence 7, Appli
14	165.5	7.2	344	2 US-08-984-207-7	Sequence 7, Appli
15	165.5	7.2	344	3 US-09-013-587-7	Sequence 7, Appli
16	165.5	7.2	344	4 US-09-086-118-27	Sequence 27, Appli
17	165.5	7.2	344	4 US-09-431-614-15	Sequence 15, Appli
18	165.5	7.2	344	5 PCT-US96-08819-7	Sequence 7, Appli
19	160.5	6.9	907	2 US-09-010-928B-4	Sequence 4, Appli
20	157.5	6.8	2870	4 US-09-479-467A-15	Sequence 15, Appli
21	157.5	6.8	3178	4 US-09-409-467A-4	Sequence 4, Appli
22	156.5	6.8	1912	1 US-08-409-995-4	Sequence 4, Appli
23	156.5	6.8	1912	3 US-08-685-467-4	Sequence 4, Appli
24	156	6.8	2039	4 US-09-077-098A-7	Sequence 7, Appli
25	155.5	6.7	2353	3 US-09-377-155-33	Sequence 33, Appli
26	155.5	6.7	2353	3 US-08-913-942-4	Sequence 4, Appli
27	155.5	6.7	2353	3 US-09-669-974-33	Sequence 33, Appli

28	155.5	6.7	2353	4 US-09-797-862-33	Sequence 33, Appli
29	155.5	6.7	2353	4 US-09-684-707-4	Sequence 4, Appli
30	155.5	6.7	2354	3 US-09-268-347-47	Sequence 47, Appli
31	155	6.7	385	5 PCT-US93-06243-2	Sequence 2, Appli
32	155	6.7	495	2 US-08-794-795-2	Sequence 2, Appli
33	155	6.7	495	3 US-09-249-200-2	Sequence 2, Appli
34	154.5	6.7	975	4 US-09-328-352-4764	Sequence 4764, Ap
35	154	6.7	571	3 US-09-134-001C-3865	Sequence 3865, Ap
36	151	6.5	385	1 US-08-891-254-3	Sequence 3, Appli
37	151	6.5	385	2 US-08-819-539-3	Sequence 3, Appli
38	151	6.5	385	5 PCT-US96-08819-3	Sequence 3, Appli
39	151	6.5	403	2 US-08-200-724A-2	Sequence 2, Appli
40	151	6.5	403	2 US-09-030-270A-3	Sequence 3, Appli
41	151	6.5	403	3 US-08-851-376A-2	Sequence 2, Appli
42	151	6.5	403	3 US-08-984-207-3	Sequence 3, Appli
43	151	6.5	403	3 US-09-013-587-3	Sequence 3, Appli
44	151	6.5	403	4 US-09-086-118-23	Sequence 23, Appli
45	151	6.5	403	4 US-09-431-614-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-120-927-2  
; Sequence 2, Application US/09120927  
; Patent No. 6262018  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jihyun Francis  
; APPLICANT: Beer, Steven V.  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Nixon, Hartgrave, Devans & Doyle LLP  
; STREET: P.O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,927  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/055,108  
; FILING DATE: 06-AUG-1977  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1581  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-120-927-2

Query Match 100.0%; Score 2310; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 5.8e-175;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNTSSPGLFQSGDNGLGHHNANSALGOQPIDRQTIEQMAQLLELLKSLLS 60

Db 1 MSILTLNNNTSSPGLFQSGDNGLGGHNANSALGQOPIDRQTIQMAQLLAELLSLIS 60  
QY 61 POSGNAATGAGGNDQTTGVNAGGLNKRGTAGTTPOSDSQNMLSEMGNNGLDQAITPDG 120  
Db 61 POSGNAATGAGGNDQTTGVNAGGLNKRGTAGTTPOSDSQNMLSEMGNNGLDQAITPDG 120  
QY 121 QCGGQIGDNPPLKAMLKLIARWMDGSDQFGPGTGNNSASSGTSSSGSPNDLSGGKA 180  
Db 121 QCGGQIGDNPPLKAMLKLIARWMDGSDQFGPGTGNNSASSGTSSSGSPNDLSGGKA 180  
QY 181 PSNGSPSGNYSVPSTFSPSTPTSPPLDFFSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
Db 181 PSNGSPSGNYSVPSTFSPSTPTSPPLDFFSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
QY 241 NSVAFTSAGANTVLHDTITVKAGQVFDGKGTFTAGSELGGGSENGKPLFILEDGAS 300  
Db 241 NSVAFTSAGANTVLHDTITVKAGQVFDGKGTFTAGSELGGGSENGKPLFILEDGAS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSKSHVEITNSSFEHASD 360  
Db 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSKSHVEITNSSFEHASD 360  
QY 361 KILQNLADTNLSVDNVKAKDPTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
Db 361 KILQNLADTNLSVDNVKAKDPTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
Db 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 2

US-09-431-614-6

; Sequence 6, Application US/09431614

; Patent No. 6624139

; GENERAL INFORMATION:

; APPLICANT: Wei, Zhong-Min

; APPLICANT: Schading, Richard L.

; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS

; TITLE OF INVENTION: RESISTANCE

; FILE REFERENCE: 21829/41 (EBC-003)

; CURRENT APPLICATION NUMBER: US/09/431,614

; CURRENT FILING DATE: 1999-11-02

; EARLIER APPLICATION NUMBER: 60/107,243

; EARLIER FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver..2.0

; SEQ ID NO 6

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Erwinia amylovora

US-09-431-614-6

Query Match 100.0%; Score 2310; DB 4; Length 447;

Best Local Similarity 100.0%; Pred. No. 5.8e-175;

Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGDNGLGGHNANSALGQOPIDRQTIQMAQLLAELLSLIS 60  
Db 1 MSILTLNNNTSSPGLFQSGDNGLGGHNANSALGQOPIDRQTIQMAQLLAELLSLIS 60  
QY 61 POSGNAATGAGGNDQTTGVNAGGLNKRGTAGTTPOSDSQNMLSEMGNNGLDQAITPDG 120  
Db 61 POSGNAATGAGGNDQTTGVNAGGLNKRGTAGTTPOSDSQNMLSEMGNNGLDQAITPDG 120  
QY 121 QCGGQIGDNPPLKAMLKLIARWMDGSDQFGPGTGNNSASSGTSSSGSPNDLSGGKA 180  
Db 121 QCGGQIGDNPPLKAMLKLIARWMDGSDQFGPGTGNNSASSGTSSSGSPNDLSGGKA 180  
QY 181 PSNGSPSGNYSVPSTFSPSTPTSPPLDFFSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
Db 181 PSNGSPSGNYSVPSTFSPSTPTSPPLDFFSSPTKAAGGTPVTDHPDPVGSAGIGAG 240

QY 241 NSVAFTSAGANTVLHDTITVKAGQVFDGKGTFTAGSELGGGSENGKPLFILEDGAS 300  
Db 241 NSVAFTSAGANTVLHDTITVKAGQVFDGKGTFTAGSELGGGSENGKPLFILEDGAS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSKSHVEITNSSFEHASD 360  
Db 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSKSHVEITNSSFEHASD 360  
QY 361 KILQNLADTNLSVDNVKAKDPTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
Db 361 KILQNLADTNLSVDNVKAKDPTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
Db 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 3

US-09-120-817-2

; Sequence 2, Application US/09120817

; Patent No. 6172184

; GENERAL INFORMATION:

; APPLICANT: Collmer, Alan

; APPLICANT: Charkowski, Amy

; APPLICANT: Alfano, James R.

; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM

; TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESS: Nixon, Hargrave, Devans & Doyle LLP

; STREET: P.O. Box 1051, Clinton Square

; CITY: Rochester

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 14603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/120,817

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/055,107

; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Goldman, Michael L.

; REGISTRATION NUMBER: 30,727

; REFERENCE/DOCKET NUMBER: 19603/1741

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (716) 263-1304

; TELEFAX: (716) 263-1600

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 424 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-120-817-2

Query Match 24.2%; Score 559; DB 3; Length 424;

Best Local Similarity 36.1%; Pred. No. 2.9e-36;

Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;

QY 37 OPIDRQTIQMAQLLAELLSLIS---LSPQSGNAATGAGGNDQTTGVNAGGLNKRGTAG 93  
Db 72 KPNDQS--NIAKULISALIMSLQMLTNSKKQDTNQPDSPQAPFQNNGLG----- 122  
QY 94 TTPQSDSQNMLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARWMDGSDQFGQP 153



Db 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151  
Qy 154 GTGNASASGTSAGSPNDLSGGKAPGNSGNYSPVSTPSPSTPTSPSPDPPS 213  
Db 152 GGDTPATGGGSGGGTPTATGG--SGGTPATGGGGGVTPTTQ-----A 200  
Qy 214 SPTKAAGGTPVTDHDPDVSAGIGAGNSVAFTSAGANQTVLHDTITVKAGQVFDGKGT 273  
Db 201 NNRTSG-----TGSVSDTAGS-----TEQAGKINNVKDTIKVGAQVFDGHTAT 245  
Qy 274 FTAGSELGCGGSENGKPLFILEDGLASLKNVTMGDDGADGHIHYG----DAKIDNLHVTN 329  
Db 246 FTADKSMGNDGQENKPFELAEAGTLKNVNLGENEVGHIHVKAKNAQEVTDNVAQN 305  
Qy 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKTLQNLADTNLSVDNVKAKDFGTFTVRTNG 389  
Db 306 VGEDLITVKGEGGAATNLNKNSSAKGADKVVQNLNANTHLKIDNFKADDFGTWRTNG 365  
Qy 390 GQO-GNWDNLNLSHSAEDGKFSVKSDEGLNVNTSDISLGDVENVH 435  
Db 366 GKQFDDMSIELNGIEANHGKFAVKSDDSLKATGNIAMTDVKHAY 412

## RESULT 4

US-09-431-614-14  
; Sequence 14, Application US/09431614  
; Patent No. 6624139  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Schading, Richard L.  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS  
; FILE OF INVENTION: RESISTANCE  
; FILE REFERENCE: 21829/41 (EBC-003)  
; CURRENT APPLICATION NUMBER: US/09/431,614  
; PRIOR FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 60/107,243  
; EARLIER FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; TYPE: PRT  
; ORGANISM: Pseudomonas syringae  
US-09-431-614-14

Query Match 24.2%; Score 559; DB 4; Length 424;  
Best Local Similarity 36.1%; Pred. No. 2.9e-36;  
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;  
Qy 37 QPIDQTISQMAQLLAELKSL---LSQSGNNAATGAGNDQTTGVGNAGLNGRKGTAG 93  
Db 72 KPNDQS--NIAKLISALIMSLLOMLTNSNKKQDTNQEOPDSQAPFQNNGLG----- 122  
Qy 94 TTPQSDSQNLSEMGNNGLDQAITPQCGGQIGDNPPLKMLKLIARMQDSQDFGQP 153  
Db 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151  
Qy 154 GTGNASASGTSAGSPNDLSGGKAPGNSGNYSPVSTPSPSTPTSPSPDPPS 213  
Db 152 GGDTPATGGGSGGGTPTATGG--SGGTPATGGGGGVTPTTQ-----A 200  
Qy 214 SPTKAAGGTPVTDHDPDVSAGIGAGNSVAFTSAGANQTVLHDTITVKAGQVFDGKGT 273  
Db 201 NNRTSG-----TGSVSDTAGS-----TEQAGKINNVKDTIKVGAQVFDGHTAT 245  
Qy 274 FTAGSELGCGGSENGKPLFILEDGLASLKNVTMGDDGADGHIHYG----DAKIDNLHVTN 329  
Db 246 FTADKSMGNDGQENKPFELAEAGTLKNVNLGENEVGHIHVKAKNAQEVTDNVAQN 305  
Qy 330 VGEDAITVKPNSAGKSHVEITNSSFEHASDKTLQNLADTNLSVDNVKAKDFGTFTVRTNG 389  
Db 306 VGEDLITVKGEGGAATNLNKNSSAKGADKVVQNLNANTHLKIDNFKADDFGTWRTNG 365

Qy 390 GQO-GNWDNLNLSHSAEDGKFSVKSDEGLNVNTSDISLGDVENVH 435  
Db 366 GKQFDDMSIELNGIEANHGKFAVKSDDSLKATGNIAMTDVKHAY 412

## RESULT 5

US-09-402-668-2  
; Sequence 2, Application US/09402668  
; Patent No. 6172030  
; GENERAL INFORMATION:  
; APPLICANT: WADA, Yasunao  
; APPLICANT: KASAI, Miyuki  
; APPLICANT: SHIKATA, Shitsuw  
; APPLICANT: SUZUMATSU, Atsushi  
; APPLICANT: KOIKE, Kenzo  
; APPLICANT: HATADA, Yuji  
; APPLICANT: KOBAYASHI, Tohru  
; APPLICANT: ITO, Susumu  
; APPLICANT: TSUMADORI, Masaki  
; TITLE OF INVENTION: Detergent Composition  
; FILE REFERENCE: 2173-0116P  
; CURRENT APPLICATION NUMBER: US/09/402,668  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 9-091142 JAPAN  
; PRIOR FILING DATE: 1997-04-09  
; PRIOR APPLICATION NUMBER: 9-242736 JAPAN  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/01613  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
; OTHER INFORMATION: Strain: KSM-P15  
US-09-402-668-2

Query Match 15.6%; Score 359.5; DB 3; Length 197;  
Best Local Similarity 46.3%; Pred. No. 6.6e-21;  
Matches 81; Conservative 29; Mismatches 56; Indels 9; Gaps 4;  
Qy 253 TVLHDTITVKAGQVFDGKGTGTAG-SELGDSGQSENQKPLFILEDGLASLKNVTMGDDGA 311  
Db 3 TVVHETIRVPAGQTFDGKQTYVANPNLTGDSQAENQKPIFRLEAGASLKNVVICAPAA 62  
Qy 312 DGIHLYGDAKIDNLHVTNVGDAITVKPNSAGKSHVEITNSSFEHASDKILQNLADTNL 371  
Db 63 DGWHCYGDCITITNVIEDVGEDALTLK--SSGT---VNISGGAAYKAYDKVFOINAAGTI 117  
Qy 372 SYDNVKAQDFGTFVRTNGGQGNWDNLNLSHSAEDGKFSVKSDE--GLNVNT 423  
Db 118 NTRNFRADDIGKLVKQNGGTTVKVMNVENCNISRVKDALTKDSTSTGRVNT 172

## RESULT 6

US-09-198-956-4  
; Sequence 4, Application US/09198956  
; Patent No. 6165769  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Lene N.  
; APPLICANT: Schuelein, Martin  
; APPLICANT: Lange, Niels Erik K.  
; APPLICANT: Bjornvad, Mads E.  
; APPLICANT: Schorrr, Kirk  
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus  
; FILE OF INVENTION: Licheniformis  
; FILE REFERENCE: 5377.200-US  
; CURRENT APPLICATION NUMBER: US/09/198,956  
; PRIOR FILING DATE: 1998-11-24  
; EARLIER APPLICATION NUMBER: 1344/97  
; EARLIER FILING DATE: 1997-11-24

EARLIER APPLICATION NUMBER: 60/067,240  
; EARLIER FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-09-198-956-4

Query Match 14.8%; Score 341; DB 3; Length 221;  
Best Local Similarity 41.7%; Pred. No. 2.3e-19;  
Matches 73; Conservative 33; Mismatches 59; Indels 10; Gaps 2;

QY 254 VLHDTITVKGQVDFGKGTFTAGSELGDSGQSENGKPLFILEDGASLKNVTMGDDGAG 313  
DB 31 VVHKTIIVKGTQYDGKRLIAGPELGDGSGQREDQKPIFKVEDGATLKNVVLGAPADG 90

QY 314 IHLYGDAKIDNLHVTNVGDAITVKNPNSAGKSHVEITNSSPEHASDKILQNLNADTNLSV 373  
DB 91 VHTYGNASINNVWEDVGEDALTVK-----SEGSVTINGSGARLAADKIFQINKASTFTV 145

QY 374 DNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLNVNTSDISL 428  
DB 146 KNFTADQGGKFIQLGGSTFKAVVINDNCTITNMKEAIFRTDS-----STSSVTM 195

RESULT 7  
US-09-670-141-4  
; Sequence 4, Application US/09670141  
; Patent No. 6429000  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Lene N.  
; APPLICANT: Schuelein, Martin  
; APPLICANT: Lange, Niels Erik K.  
; APPLICANT: Bjornvad, Mads E.  
; APPLICANT: Schnorr, Kirk  
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus  
; FILE REFERENCE: 5377,200-US  
; CURRENT APPLICATION NUMBER: US/09/670,141  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: 09/198,956  
; PRIOR FILING DATE: 1998-11-24  
; PRIOR APPLICATION NUMBER: 1344/97  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/067,240  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-09-670-141-4

Query Match 14.8%; Score 341; DB 4; Length 221;  
Best Local Similarity 41.7%; Pred. No. 2.3e-19;  
Matches 73; Conservative 33; Mismatches 59; Indels 10; Gaps 2;

QY 254 VLHDTITVKGQVDFGKGTFTAGSELGDSGQSENGKPLFILEDGASLKNVTMGDDGAG 313  
DB 31 VVHKTIIVKGTQYDGKRLIAGPELGDGSGQREDQKPIFKVEDGATLKNVVLGAPADG 90

QY 314 IHLYGDAKIDNLHVTNVGDAITVKNPNSAGKSHVEITNSSPEHASDKILQNLNADTNLSV 373  
DB 91 VHTYGNASINNVWEDVGEDALTVK-----SEGSVTINGSGARLAADKIFQINKASTFTV 145

QY 374 DNVKAKDFGTFVRTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLNVNTSDISL 428  
DB 146 KNFTADQGGKFIQLGGSTFKAVVINDNCTITNMKEAIFRTDS-----STSSVTM 195

RESULT 8  
US-09-402-668-10  
; Sequence 10, Application US/09402668  
; Patent No. 6172030  
; GENERAL INFORMATION:  
; APPLICANT: WADA, Yasunao  
; APPLICANT: KASAI, Miyuki  
; APPLICANT: SHIKATA, Shitsuw  
; APPLICANT: SUZUMATSU, Atsushi  
; APPLICANT: KOIKE, Kenzo  
; APPLICANT: HATADA, Yuji  
; APPLICANT: KOBAYASHI, Tohru  
; APPLICANT: ITO, Susumu  
; APPLICANT: TSUMADORI, Masaki  
; TITLE OF INVENTION: Detergent Composition  
; FILE REFERENCE: 2173-0116P  
; CURRENT APPLICATION NUMBER: US/09/402,668  
; CURRENT FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 9-091142 JAPAN  
; PRIOR FILING DATE: 1997-04-09  
; PRIOR APPLICATION NUMBER: 9-242736 JAPAN  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/01613  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide from  
; OTHER INFORMATION: primer  
US-09-402-668-10

Query Match 8.2%; Score 190.5; DB 3; Length 62;  
Best Local Similarity 65.0%; Pred. No. 3.3e-08;  
Matches 39; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 253 TVLHDTITVKGQVDFGKGTFTAG-SELGDSGQSENGKPLFILEDGASLKNVTMGDDGA 311  
DB 3 TVVHETIRVAGQTFDGKGTIVVNPNTLGDGSAENKPIFLRLEAGASLKNVVGAPAA 62

RESULT 9  
US-09-268-347-36  
; Sequence 36, Application US/09268347  
; Patent No. 6335182  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS  
; FILE REFERENCE: 1038-860  
; CURRENT APPLICATION NUMBER: US/09/268,347  
; CURRENT FILING DATE: 1999-03-16  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 2411  
; TYPE: PRT  
; ORGANISM: Haemophilus influenzae  
US-09-268-347-36

Query Match 7.9%; Score 181.5; DB 3; Length 2411;  
Best Local Similarity 20.6%; Pred. No. 2.6e-05;  
Matches 126; Conservative 64; Mismatches 205; Indels 217; Gaps 26;

QY 4 LTINN-----NTSSSPGLFQSGGDNGLGHN-----ANSALGOPIDROT 43  
DB 1182 ITLANGAAGTDAISNGTISVTGKGLISAGNKEITNVKSALKTYKDTQNTAGATQPA-ANT 1240

QY 44 IEQMAQLLAELKSLISPOSNAATCAGGNDOTTGVGNAGGLNG-----RKGTAGTTTPO 97  
DB 1241 AEVAKQDLVDLTK----PATGAAGNGADAKAPDTTAAATVGLRGLGWLSAKKTADETQD 1296

Query Match 7.9%; Score 181.5; DB 3; Length 2411;  
Best Local Similarity 20.6%; Pred. No. 2.6e-05;  
Matches 126; Conservative 64; Mismatches 205; Indels 217; Gaps 26;

QY 4 LTINN-----NTSSSPGLFQSGGDNGLGHN-----ANSALGOPIDROT 43  
DB 1182 ITLANGAAGTDAISNGTISVTGKGLISAGNKEITNVKSALKTYKDTQNTAGATQPA-ANT 1240

QY 44 IEQMAQLLAELKSLISPOSNAATCAGGNDOTTGVGNAGGLNG-----RKGTAGTTTPO 97  
DB 1241 AEVAKQDLVDLTK----PATGAAGNGADAKAPDTTAAATVGLRGLGWLSAKKTADETQD 1296



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,254  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-891-254-7

Query Match 7.2%; Score 165.5; DB 1; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.3e-05;  
Matches 57; Conservative 20; Mismatches 80; Indels 21; Gaps 7;

QY 18 QSGGD---NGLGHNANSALGQPIDROTIEQMAQLLAEL-LKSLSPQSGNAATGAGN 73  
DB 134 QPGNDKNGVGGANGAKGAGGGGLAEALQIEQLAQLGGGAGAGGAGGAGGAGGA 193  
QY 74 DDTTGVNAGLNGRGKTAGT--TPQSDSQNMLSEMGNGLDQAITPDG--QGGGQIGDN 129  
DB 194 DGGGAGGAGGANGADGGNGVNGNQANGPQNGADVNGANGAD-----DGSEDDQGLTGVL 248  
QY 130 PLLKAMKLIAEMD-----QSDQFQPGPTGNNSSAGTSSSGGSP--FNDLSGGK 179  
DB 249 QKLAKILNALVQMGGGLGGNQAGGSKGAGNAPASGANPGANQPGSADDDSSGQ 306

RESULT 12  
US-08-819-539-7  
Sequence 7, Application US/08819539  
Patent No. 5859324  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response  
TITLE OF INVENTION: Induced Resistance In Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,539  
FILING DATE: 17-MAR-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-819-539-7

Query Match 7.2%; Score 165.5; DB 2; Length 344;  
Best Local Similarity 32.0%; Pred. No. 3.3e-05;  
Matches 57; Conservative 20; Mismatches 80; Indels 21; Gaps 7;

QY 18 QSGGD---NGLGHNANSALGQPIDROTIEQMAQLLAEL-LKSLSPQSGNAATGAGN 73  
DB 134 QPGNDKNGVGGANGAKGAGGGGLAEALQIEQLAQLGGGAGAGGAGGAGGAGGA 193  
QY 74 DDTTGVNAGLNGRGKTAGT--TPQSDSQNMLSEMGNGLDQAITPDG--QGGGQIGDN 129  
DB 194 DGGGAGGAGGANGADGGNGVNGNQANGPQNGADVNGANGAD-----DGSEDDQGLTGVL 248  
QY 130 PLLKAMKLIAEMD-----QSDQFQPGPTGNNSSAGTSSSGGSP--FNDLSGGK 179  
DB 249 QKLAKILNALVQMGGGLGGNQAGGSKGAGNAPASGANPGANQPGSADDDSSGQ 306

RESULT 13  
US-09-030-270A-7  
Sequence 7, Application US/09030270A  
Patent No. 5977060  
GENERAL INFORMATION:  
APPLICANT: Zitter, Thomas A.  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: INSECT CONTROL WITH A  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,270A  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,226  
FILING DATE: 28-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids

; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-030-270A-7

Query Match 7.2%; Score 165.5; DB 2; Length 344;  
 Best Local Similarity 32.0%; Pred. No. 3.3e-05;  
 Matches 57; Conservative 20; Mismatches 80; Indels 21; Gaps 7;

QY 18 QSGGD---NGLGHNANSALGQPIDRTIEQMAQLLAE-LKSLSPSGNAATGAGN 73  
 Db 134 QPGNDKNGVGGANGAKGAGGGGLAEALQIEIQLAQLGGGAGAGGGVGGAGA 193  
 QY 74 DQTTGVNAGGLNGRKGTAGT--TPQSDSQNMLSEMGNNGLDQAITPDG--QGGGGIGDN 129  
 Db 194 DGGSGAGGAGGAGDGGNGVNGNQANGPQNGADVNGANGAD-----DGSDDGGGLTGV 248  
 QY 130 PLLKAWMLKLIARMMD-----QSDQFQPGQGTGNNSSASSTSSGGSP--FNDLSGK 179  
 Db 249 QKLMKILNALVQMVGGLGGNGNQAGGSKGAGNAPASGANPGANPGSADDDQSSGQ 306

## RESULT 14

US-08-984-207-7  
 ; Sequence 7, Application US/08984207  
 ; Patent No. 6235974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Qiu, Dewen  
 ; APPLICANT: Wei, Zhong-Min  
 ; APPLICANT: Beer, Steven V.  
 ; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
 ; TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: P.O. Box 1051, Clinton Square  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/984,207  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/033,230  
 ; FILING DATE: 05-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldman, Michael L.  
 ; REGISTRATION NUMBER: 30,727  
 ; REFERENCE/DOCKET NUMBER: 19603/1201  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1304  
 ; TELEFAX: (716) 263-1600  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 344 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

Query Match 7.2%; Score 165.5; DB 3; Length 344;  
 Best Local Similarity 32.0%; Pred. No. 3.3e-05;  
 Matches 57; Conservative 20; Mismatches 80; Indels 21; Gaps 7;

QY 18 QSGGD---NGLGHNANSALGQPIDRTIEQMAQLLAE-LKSLSPSGNAATGAGN 73  
 Db 134 QPGNDKNGVGGANGAKGAGGGGLAEALQIEIQLAQLGGGAGAGGGVGGAGA 193  
 QY 74 DQTTGVNAGGLNGRKGTAGT--TPQSDSQNMLSEMGNNGLDQAITPDG--QGGGGIGDN 129  
 Db 194 DGGSGAGGAGGAGDGGNGVNGNQANGPQNGADVNGANGAD-----DGSDDGGGLTGV 248  
 QY 130 PLLKAWMLKLIARMMD-----QSDQFQPGQGTGNNSSASSTSSGGSP--FNDLSGK 179  
 Db 249 QKLMKILNALVQMVGGLGGNGNQAGGSKGAGNAPASGANPGANPGSADDDQSSGQ 306

## RESULT 15

US-09-013-587-7  
 ; Sequence 7, Application US/09013587  
 ; Patent No. 6277814  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Qiu, Dewen  
 ; APPLICANT: Wei, Zhong-Min  
 ; APPLICANT: Beer, Steven V.  
 ; TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/013,587  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/036,048  
 ; FILING DATE: 27-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldman, Michael L.  
 ; REGISTRATION NUMBER: 30,727  
 ; REFERENCE/DOCKET NUMBER: 19603/1501  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1304  
 ; TELEFAX: (716) 263-1600  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 344 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

Query Match 7.2%; Score 165.5; DB 3; Length 344;  
 Best Local Similarity 32.0%; Pred. No. 3.3e-05;  
 Matches 57; Conservative 20; Mismatches 80; Indels 21; Gaps 7;

QY 18 QSGGD---NGLGHNANSALGQPIDRTIEQMAQLLAE-LKSLSPSGNAATGAGN 73  
 Db 134 QPGNDKNGVGGANGAKGAGGGGLAEALQIEIQLAQLGGGAGAGGGVGGAGA 193  
 QY 74 DQTTGVNAGGLNGRKGTAGT--TPQSDSQNMLSEMGNNGLDQAITPDG--QGGGGIGDN 129  
 Db 194 DGGSGAGGAGGAGDGGNGVNGNQANGPQNGADVNGANGAD-----DGSDDGGGLTGV 248  
 QY 130 PLLKAWMLKLIARMMD-----QSDQFQPGQGTGNNSSASSTSSGGSP--FNDLSGK 179  
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Search completed: January 25, 2005, 16:10:54  
Job time : 42 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 16:09:28 ; Search time 149 Seconds  
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1083.868 Million cell updates/sec

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Perfect score: 2310  
Sequence: 1 MSILTLNNTSSPGLFQSG.....LGDVENHYKVPMSANLKVAE 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2310	100.0	447	9	US-09-835-684-5
2	2310	100.0	447	9	US-09-880-371-5
3	2310	100.0	447	9	US-09-879-248-6
4	2310	100.0	447	14	US-10-010-390-5
5	2310	100.0	447	15	US-10-441-736-6
6	2310	100.0	447	17	US-10-847-142-5
7	559	24.2	424	9	US-09-835-684-9
8	559	24.2	424	9	US-09-880-371-9
9	559	24.2	424	9	US-09-879-248-14
10	559	24.2	424	14	US-10-010-390-9
11	559	24.2	424	15	US-10-441-736-14
12	559	24.2	424	17	US-10-847-142-9
13	256	11.1	276	14	US-10-156-761-13910

14	199.5	8.6	1306	15	US-10-282-122A-64405	Sequence 64405, A
15	193	8.4	694	15	US-10-282-122A-64726	Sequence 64726, A
16	191.5	8.3	584	15	US-10-282-122A-50604	Sequence 50604, A
17	190.5	8.2	226	17	US-10-425-115-229387	Sequence 229387, A
18	188	8.1	639	15	US-10-282-122A-64609	Sequence 64609, A
19	186.5	8.1	591	15	US-10-282-122A-64363	Sequence 64363, A
20	185.5	8.0	1381	15	US-10-282-122A-64895	Sequence 64895, A
21	185	8.0	255	17	US-10-425-115-313677	Sequence 313677, A
22	183	7.9	588	15	US-10-282-122A-64869	Sequence 64869, A
23	182	7.9	606	15	US-10-282-122A-64464	Sequence 64464, A
24	181.5	7.9	484	10	US-09-820-843A-19	Sequence 19, Appl
25	181.5	7.9	484	15	US-10-282-122A-64867	Sequence 64867, A
26	180.5	7.8	1079	10	US-09-820-843A-20	Sequence 20, Appl
27	176.5	7.6	562	15	US-10-282-122A-64514	Sequence 64514, A
28	174	7.5	615	15	US-10-282-122A-64786	Sequence 64786, A
29	174	7.5	2042	14	US-10-192-584-6	Sequence 6, Appl1
30	172.5	7.5	584	15	US-10-282-122A-64903	Sequence 64903, A
31	172	7.4	3507	14	US-10-369-493-5784	Sequence 5784, Ap
32	171.5	7.4	667	15	US-10-282-122A-64494	Sequence 64494, A
33	171	7.4	505	15	US-10-282-122A-62341	Sequence 62341, A
34	169.5	7.3	914	15	US-10-282-122A-64606	Sequence 64606, A
35	169	7.3	525	15	US-10-282-122A-64763	Sequence 64763, A
36	167.5	7.3	1011	15	US-10-282-122A-64589	Sequence 64589, A
37	166.5	7.2	518	15	US-10-282-122A-50634	Sequence 50634, A
38	166.5	7.2	532	15	US-10-282-122A-64658	Sequence 64658, A
39	166	7.2	461	15	US-10-282-122A-64750	Sequence 64750, A
40	166	7.2	603	15	US-10-282-122A-64537	Sequence 64537, A
41	166	7.2	767	15	US-10-282-122A-48384	Sequence 48384, A
42	165.5	7.2	344	9	US-09-086-118-27	Sequence 27, Appl
43	165.5	7.2	344	9	US-09-835-684-11	Sequence 11, Appl
44	165.5	7.2	344	9	US-09-880-371-11	Sequence 11, Appl
45	165.5	7.2	344	9	US-09-879-248-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-835-684-5  
; Sequence 5, Application US/09835684  
; Patent No. US20020019337A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Qiu, Dewen  
; APPLICANT: Remick, Dean  
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR DESICCATION  
; TITLE OF INVENTION: DESICCATION  
; FILE REFERENCE: 21829/71  
; CURRENT APPLICATION NUMBER: US/09/835,684  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/198,359  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
US-09-835-684-5

Query Match	100.0%	Score 2310;	DB 9;	Length 447;
Best Local Similarity	100.0%	Pred. No. 1.4e-151;		
Matches 447;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MSILTLNNTSSPGLFQSGDNGLGGHNANSALGQOPIDROTITQMAOLLAEKLSLS	60	
Oy	61	POSGNAATGAGGNDOTTGVGNAGGNGRKGTTAGTTPQSDSQNMLSEMGNGLDQAITPDG	120	
Db	61	POSGNAATGAGGNDOTTGVGNAGGNGRKGTTAGTTPQSDSQNMLSEMGNGLDQAITPDG	120	

QY 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
DB 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
QY 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
DB 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
QY 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
DB 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

## RESULT 2

US-09-880-371-5  
; Sequence 5, Application US/09880371  
; Patent No. US20020059658A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: DeRoche, Jay  
; TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 21829/91  
; CURRENT APPLICATION NUMBER: US/09/880,371  
; CURRENT FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/211,585  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
US-09-880-371-5

Query Match 100.0%; Score 2310; DB 9; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSSPGLFQSGGDNGLGHNANSALGOQPIDROTIEQMAQLLAELLKSLLS 60  
DB 1 MSILTLNNNTSSSPGLFQSGGDNGLGHNANSALGOQPIDROTIEQMAQLLAELLKSLLS 60  
QY 61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTQSDSQNMLSEMNGNGLDQAITPDG 120  
DB 61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTQSDSQNMLSEMNGNGLDQAITPDG 120  
QY 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
DB 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
QY 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
DB 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360

DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
QY 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
DB 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

## RESULT 3

US-09-879-248-6  
; Sequence 6, Application US/09879248  
; Patent No. US20020062500A1  
; GENERAL INFORMATION:  
; APPLICANT: Fan, Hao  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 21829/81  
; CURRENT APPLICATION NUMBER: US/09/879,248  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: 60/212,211  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
US-09-879-248-6

Query Match 100.0%; Score 2310; DB 9; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.4e-151;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSSPGLFQSGGDNGLGHNANSALGOQPIDROTIEQMAQLLAELLKSLLS 60  
DB 1 MSILTLNNNTSSSPGLFQSGGDNGLGHNANSALGOQPIDROTIEQMAQLLAELLKSLLS 60  
QY 61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTQSDSQNMLSEMNGNGLDQAITPDG 120  
DB 61 PQSGNAATGAGGNDQTTGVNAGGLNGRGTAGTTTQSDSQNMLSEMNGNGLDQAITPDG 120  
QY 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
DB 121 OGGGQIGDNPLLKAMLKLIARMDGSDQFQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180  
QY 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
DB 181 PSGNSPGNYSVPSTFSPSTPTSPPLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG 240  
QY 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
DB 241 NSVAFTSAGANQTVLHDTITVKAGQVFDGKGOTFTAGSELGCGGQSENOKPLFILEDGAS 300  
QY 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
DB 301 LKNVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFEHSD 360  
QY 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
DB 361 KILQNLNADTNLSVDNVKAKDFGTFTVTNGGQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420  
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447  
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

## RESULT 4

US-10-010-390-5  
; Sequence 5, Application US/10010390



```
; Publication No. US20030104979A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Leon, Ernesto
; APPLICANT: Oviedo, Agustin
; TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
; TITLE OF INVENTION: FROM ORNAMENTAL PLANTS
; FILE REFERENCE: 21829/111
; CURRENT APPLICATION NUMBER: US/10/010,390
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/248,169
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-010-390-5

Query Match 100.0%; Score 2310; DB 14; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.4e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
DB 1 MSILTLNNNTSSPGLFQSGGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
QY 61 POSGNAATGAGGNDQTTGVNAGLNGRKGTTAGTTTPOSQSNMLSEMGNGLDQAITPDG 120
DB 61 POSGNAATGAGGNDQTTGVNAGLNGRKGTTAGTTTPOSQSNMLSEMGNGLDQAITPDG 120
QY 121 QGGGQIGDNPLLKAMLKLIARWMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180
DB 121 QGGGQIGDNPLLKAMLKLIARWMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180
QY 181 PSNGSPSGNYSVPSTPSTPTSPPLDFFSSPTKAAGGTPVTDHDPVGSAGIGAG 240
DB 181 PSNGSPSGNYSVPSTPSTPTSPPLDFFSSPTKAAGGTPVTDHDPVGSAGIGAG 240
QY 241 NSVAFTSAGANQTVLHDTITVRAGQVFDGKGOTFTAGSELGQGGQSENOKPLFILEDGAS 300
DB 241 NSVAFTSAGANQTVLHDTITVRAGQVFDGKGOTFTAGSELGQGGQSENOKPLFILEDGAS 300
QY 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGSDAITVKPNSAGKSKSHVEITNSSPEHSD 360
DB 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGSDAITVKPNSAGKSKSHVEITNSSPEHSD 360
QY 361 KILQLNADTNLSVDNVKAKDFGTFTVTNGQQQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420
DB 361 KILQLNADTNLSVDNVKAKDFGTFTVTNGQQQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 5
US-10-441-736-6
; Sequence 6, Application US/10441736
; Publication No. US20040016029A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Remick, Dean
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/203 (EBC-003)
; CURRENT APPLICATION NUMBER: US/10/441,736
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/107,243
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/431,614
; PRIOR FILING DATE: 1999-11-02

; Publication No. US20030104979A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Leon, Ernesto
; APPLICANT: Oviedo, Agustin
; TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
; TITLE OF INVENTION: FROM ORNAMENTAL PLANTS
; FILE REFERENCE: 21829/111
; CURRENT APPLICATION NUMBER: US/10/010,390
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/248,169
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-441-736-6

Query Match 100.0%; Score 2310; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.4e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSILTLNNNTSSPGLFQSGGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
DB 1 MSILTLNNNTSSPGLFQSGGDNGLGHNANSALGQOPIIDROTIEQMAQLLAELLKSLLS 60
QY 61 POSGNAATGAGGNDQTTGVNAGLNGRKGTTAGTTTPOSQSNMLSEMGNGLDQAITPDG 120
DB 61 POSGNAATGAGGNDQTTGVNAGLNGRKGTTAGTTTPOSQSNMLSEMGNGLDQAITPDG 120
QY 121 QGGGQIGDNPLLKAMLKLIARWMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180
DB 121 QGGGQIGDNPLLKAMLKLIARWMDGQSDQFGQPGTGNNSSASGTSSSGSGSPFNDLSGGKA 180
QY 181 PSNGSPSGNYSVPSTPSTPTSPPLDFFSSPTKAAGGTPVTDHDPVGSAGIGAG 240
DB 181 PSNGSPSGNYSVPSTPSTPTSPPLDFFSSPTKAAGGTPVTDHDPVGSAGIGAG 240
QY 241 NSVAFTSAGANQTVLHDTITVRAGQVFDGKGOTFTAGSELGQGGQSENOKPLFILEDGAS 300
DB 241 NSVAFTSAGANQTVLHDTITVRAGQVFDGKGOTFTAGSELGQGGQSENOKPLFILEDGAS 300
QY 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGSDAITVKPNSAGKSKSHVEITNSSPEHSD 360
DB 301 LKNVTMGDDGADGIHLGYDAKIDNLHVTNVGSDAITVKPNSAGKSKSHVEITNSSPEHSD 360
QY 361 KILQLNADTNLSVDNVKAKDFGTFTVTNGQQQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420
DB 361 KILQLNADTNLSVDNVKAKDFGTFTVTNGQQQGNWDLNLSHISAEDGKFSFVKSDSEGLN 420
QY 421 VNTSDISLGDVENHYKVPMSANLKVAE 447
DB 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 6
US-10-847-142-5
; Sequence 5, Application US/10847142
; Publication No. US2004040265442A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Qiu, Dewen
; APPLICANT: Remick, Dean
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
; TITLE OF INVENTION: DESICCATION
; FILE REFERENCE: 21829/197
; CURRENT APPLICATION NUMBER: US/10/847,142
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/198,359
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/835,684
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-847-142-5

Query Match 100.0%; Score 2310; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.4e-151;
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Matches	447;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
1	MSILTLNNNTSSSPGLFQSGDNGLGGHNANALGOQPIDRQTIEQMAQLLAELLKSLLS	60							
1	MSILTLNNNTSSSPGLFQSGDNGLGGHNANALGOQPIDRQTIEQMAQLLAELLKSLLS	60							
61	POSGNAATGAGGNDQTTGVGNAGGLNGRGTAGTTPOSDSQNMLESMNGNGLDQAITPDG	120							
61	POSGNAATGAGGNDQTTGVGNAGGLNGRGTAGTTPOSDSQNMLESMNGNGLDQAITPDG	120							
121	QGGSGIQGDNPLLKAMLLKLIARMMDGSDQFGQPGTGNNSSASGTSSSGGSPENDLSGGKA	180							
121	QGGSGIQGDNPLLKAMLLKLIARMMDGSDQFGQPGTGNNSSASGTSSSGGSPENDLSGGKA	180							
181	PSGNPSGNTSPVSTSPSTPTSPDLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG	240							
181	PSGNPSGNTSPVSTSPSTPTSPDLDFPSSPTKAAGGTPVTDHPDPVGSAGIGAG	240							
241	NSVAFTSAGANQTVLHDITIIVKAGQVDFGKGQFTTAGSELGDDGGOSEKQPLFIELEDGAS	300							
241	NSVAFTSAGANQTVLHDITIIVKAGQVDFGKGQFTTAGSELGDDGGOSEKQPLFIELEDGAS	300							
301	LKNVTMGDDGADGTHLYGDADKIDNLNHLVTNVGEDAITVKPNSAKGKSHVEITNNSPEHASD	360							
301	LKNVTMGDDGADGTHLYGDADKIDNLNHLVTNVGEDAITVKPNSAKGKSHVEITNNSPEHASD	360							
361	KILQLNADTNLSVDNVKAKDFGTVRTNGGQQGNWDNLNLSHTSAEDCKGKSFVKYSSEGLN	420							
361	KILQLNADTNLSVDNVKAKDFGTVRTNGGQQGNWDNLNLSHTSAEDCKGKSFVKYSSEGLN	420							
421	VNTSDISLGDVENHYKVPMSANLKVAE	447							
421	VNTSDISLGDVENHYKVPMSANLKVAE	447							

RESULT 7  
 US-09-835-684-9  
 ; Sequence 9, Application US/09835684  
 ; Patent No. US20020019337A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wei, Zhong-Min  
 ; APPLICANT: Qiu, Dewen  
 ; APPLICANT: Remick, Dean  
 ; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE  
 ; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR  
 ; TITLE OF INVENTION: DESICCATION  
 ; FILE REFERENCE: 21829/71  
 ; CURRENT APPLICATION NUMBER: US/09/835,684  
 ; CURRENT FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: 60/198,359  
 ; PRIOR FILING DATE: 2000-04-19  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentin ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 424  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas syringae  
 US-09-835-684-9

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152 GDBTPTATGGGGGGGTATATGG---SGGTPATGGGGGVTQITPOL-----A 200
214 SPTKAAGGSTPVTDHPDPVGSAGIAGNSVAFTSAGANOTVLHDTITVKAGQVFDKGQOT 273
201 NPNRTSG-----TGSVSDTAGS-----TEQAGKINNVVKDKTIKVGAGEVFDGHGAT 245
274 FTAGSELGDSGQSEOKPLFILEDGASLKNVTMGDDGADGIHLG----DAKIDNLHVTN 329
246 FTADKSMGNGDQGENOKPFELAEAGATLKNVLGENEVDGIHVAKNAQAEVTDINVHAQN 305
330 VGEDAITVTPNSAGKSHVEITNSSFEPHASDKILQLNADNTNLSVDNVKAKDPGTFVVRTNG 389
306 VGEDLITVKGEGAAVTNLNKNSSAKGADDKVQVLNANTHLKIDNFKADDGFTGVMVRTNG 365
390 GQQ-GWNDLNLSHISAEDGKFSPVKSDEGLNVNTSDISLGDVENHY 435
366 GKQFDDMSITELNGIEANHGKFALVKSDSDDLKLATGNIAMTQVKKHAY 412

RESULT 8
US-09-880-371-9
; Sequence 9, Application US/09880371
; Patent No. US20020059658A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: DeRocher, Jay
; TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 21829/91
; CURRENT APPLICATION NUMBER: US/09/880, 371
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,585
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-09-880-371-9

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Query Match	24.28;	Score	559;	DB	9;	Length	424;
Best Local Similarity	36.18;	Pred. No.	1.9e-30;				
Matches	147;	Conservative	54;	Mismatches	132;	Indels	74;
Gaps	13;						
Qy	37	QPIDRQTEIQMAQLLAELLKSL---	LSPOSGNAATAGGNDQTTGVGNAGGLNKRKGTAG	93			
Db	72	KPNDSQS--NIAKLISALIMSLQLMTSNKKQDITNQEQPDSOAPFONNGGLG-----	122				
Qy	94	TTPOSDSQNMLSGNGNGLDQAITPDQGGGGQIGDNPLLKAMLKLIARMMDGQSDQFGQP	153				
Db	123	-TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG	151				
Qy	154	GTGNNSASSGTSSSGGSPFNDLGGKAPSGNSPFGNSYSPVTSPPSTPTSPSPDLDFPS	213				
Db	152	GGDTPTATGGGSGGGTPTATGGG---SGGTTATGGGGVTPQTTPOL-----A	200				
Qy	214	SPTKAAGGSTVTDHPDPVGSAGICAGNSVAFTSAGANQTVLHDTITVRKAGQVDFGKGQT	273				
Db	201	NPNETSG-----TGSVSDTAGS---TEQACKINVVKDTIKVGAGEVDFDGHGAT	245				
Qy	274	FTAGSELGDSGQSENOKPLFILEDGASIKNVWTCDDGADGHLXG-----DAKIDNLHVTN	329				
Db	246	FTADKSMNGDQGNQKQMPFELAGATIKNNVLGENEVGDIHVKAKNAQEVITDINVAHQN	305				
Qy	330	VGEDAITYKPNKSAGKSHVEITNSSPFHASDKILQLNADTNLSVDNVKAKDFGTFVETNG	389				
Db	306	VGEDLIITVKGGGAAVNTNLNKNSSAKGADDKVQVLNANTHLKIDNFKADDFGTMVETNG	365				
Qy	390	QQQ--GNMDLNLSHLSAEDGFSPFKVSDSEGLNVNNTSDISLDGVENHY	435				
Db	366	GKQFPDDMSIELNGEANHGFALVKSDSDDLKATGNIAMTVDVKHAY	412				



Db 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151  
Qy 154 GTGNNSASGTSSSGGSPFNDLSGKAPSGNSPNSVSPSTPSTPTSPSTPLDPPS 213  
Db 152 GGDTPATATGGGGGGGTPATGGG---SGGTPATGGGGGVTPTQITPOL-----A 200  
Qy 214 SPTKAAGSTPTVTHDPDPVGSAGIGAGNSVAFSAGANQTVLHDTITVKAGOVDPKGQT 273  
Db 201 NPNRTSG-----TGSVSDTAGS-----TEQAGKINVVKDTIKVAGEVFDHGAT 245  
Qy 274 FTAGSELGCGQSENOKPLFILEDGASLKNVTMTGDDGADGIHLYG-----DAKIDNLHVTN 329  
Db 246 FTADKSMGNDGQENQKPMFELAEATLKNVNLGENEVDGIHVAKNAQEVITDINVHAQN 305  
Qy 330 VGEDAITVKPNSAGKSHVEITNSSFEHASKILOLNADTNLSVDNVKAKDGTFTVRING 389  
Db 306 VGEDLITVKEGGAATVNLNKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTWVRTNG 365  
Qy 390 GOQ-GNWDNLNLSHSAEDGKFSFKVSDSEGLNVNTSDISLGDVENHY 435  
Db 366 GKOFDDMSIELNGIEANHGKFPALVKSDSDDLKLATGNIAMTDVKHAY 412

## RESULT 12

US-10-847-142-9  
; Sequence 9, Application US/10847142  
; Publication No. US20040265442A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Qiu, Dewen  
; APPLICANT: Remick, Dean  
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE  
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR  
; FILE OF INVENTION: DESICCATION  
; FILE REFERENCE: 21829/197  
; CURRENT APPLICATION NUMBER: US/10/847,142  
; PRIOR FILING DATE: 2004-05-17  
; PRIOR APPLICATION NUMBER: 60/198,359  
; PRIOR FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 09/935,684  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Pseudomonas syringae  
US-10-847-142-9

Query Match 24.2%; Score 559; DB 17; Length 424;  
Best Local Similarity 36.1%; Pred. No. 1.9e-30;  
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;  
Qy 37 QPIDRQTEIOMACLAELKSL---LSPOSGNAATGAGNDQTTGVGNAGGLNGRKG TAG 93  
Db 72 KPNDQSQ--NIAKLISALIMSLQMLTNSNKKQDTNQEOPDSQAPFQNNGLG-----122  
Qy 94 TTPQSDSONMLSENGNLDQAITPDQGGGQIGDNPLLKAMLKLIARWMDGSDQDQGP 153  
Db 123 -TPSADS-----GGGG-----TPDATGGG-GDTP-----SATGGG 151  
Qy 154 GTGNNSASGTSSSGGSPFNDLSGKAPSGNSPNSVSPSTPSTPTSPSTPLDPPS 213  
Db 152 GGDTPATATGGGGGGGTPATGGG---SGGTPATGGGGGVTPTQITPOL-----A 200  
Qy 214 SPTKAAGSTPTVTHDPDPVGSAGIGAGNSVAFSAGANQTVLHDTITVKAGOVDPKGQT 273  
Db 201 NPNRTSG-----TGSVSDTAGS-----TEQAGKINVVKDTIKVAGEVFDHGAT 245  
Qy 274 FTAGSELGCGQSENOKPLFILEDGASLKNVTMTGDDGADGIHLYG-----DAKIDNLHVTN 329  
Db 246 FTADKSMGNDGQENQKPMFELAEATLKNVNLGENEVDGIHVAKNAQEVITDINVHAQN 305

Qy 330 VGEDAITVKPNSAGKSHVEITNSSFEHASKILOLNADTNLSVDNVKAKDGTFTVRING 389  
Db 306 VGEDLITVKEGGAATVNLNKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTWVRTNG 365  
Qy 390 GOQ-GNWDNLNLSHSAEDGKFSFKVSDSEGLNVNTSDISLGDVENHY 435  
Db 366 GKOFDDMSIELNGIEANHGKFPALVKSDSDDLKLATGNIAMTDVKHAY 412

## RESULT 13

US-10-156-761-13910  
; Sequence 13910, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-282  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 13910  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-13910

Query Match 11.1%; Score 256; DB 14; Length 276;  
Best Local Similarity 31.7%; Pred. No. 1e-09;  
Matches 76; Conservative 35; Mismatches 87; Indels 42; Gaps 7;

Qy 225 VTDHPDPVGS---GIGAGNSVA---FTSAGANQTVLHDT-----ITVKAGQVDPDGKQ 272  
Db 15 VTKRAVIGSAALGLTAGLVTTLSAGAGATSWPEATGSKAVSSIEVSGTYDGKLLK 74  
Qy 273 TFTAGSELGCGQSENQKPLFILEDGASLKNVTMTGDDGADGIHLYGDAKIDNLHVTNVE 332  
Db 75 KFGSGDLGTADQSDQGLPELDGAVLKNVIIGTPAADGVHCLGSCCTLQNVWMLDVE 134  
Qy 333 DAITVKPNSAGKSHVEITNSSFEHASKILOLNADTNLSVDNVKAKDGTFTVRINGGQO 392  
Db 135 DAASFPSKSS--SATYKVIIGGAKSADKVLQFNGAGTLTGTGQVENFGKLVRSQCNCK 192  
Qy 393 GNWDNLNLSHSAEDGKFSFKVSDSE-----GLNVNTSDISL-----GDVENHYK 436  
Db 193 TQY-----KFTVVLSDIDATAPGKALVGINSGYGTATLSRIIHGDTKKIK 240

## RESULT 14

US-10-282-122A-64405  
; Sequence 64405, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.

APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 64405  
LENGTH: 1306  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-10-282-122A-64405

Query Match 8.6%; Score 199.5; DB 15; Length 1306;  
Best Local Similarity 26.0%; Pred. No. 5.8e-05;  
Matches 88; Conservative 16; Mismatches 122; Indels 113; Gaps 11;  
QY 8 NNTSSPGUFGSGDNGLNHNSALGQOPIDROTIEQMAQLLAELLSLSPSGNAA 67  
Db 754 NGVAGSQPGAGGDTGTGGVGGNGRIGDADGAT----- 789  
QY 68 TGAGGNDOTGVGNAGLNGKTAGTTQSDSQNMLSEWNGNGLDQAITPDGQGGQIG 127  
Db 790 --AGARGQDGGAGGAGKGRGTGTP-----GGAGPAGTTGSGAGGNG 832  
QY 128 DNPLLKAMLKLIARMMDQSDQDFGQPGTGNNSASGTSPPNDLSGCKA--PSGNSP 186  
Db 833 -----GSGGTGDDPCDGNANGSVFTNNGIGNGGNGGNGSLRG 875  
QY 187 SGNYSPVSTPSPPTSPSPL-----DFPSPTKAAG-----G 221  
Db 876 SGAG--STFG---ATGSSSIHVNGCGNGGNGDHALSGAAGCGNGGSLRG 929  
QY 222 STPVTDHPVGSAGTIGANSVAFPSAGANQTVLHDTITVKAGQVFDGKQFTTAGSELG 281  
Db 930 SGAGGHGNGGNASRGMGDDGTGAGGN-----AGQITNG-----GAGGNGG 973  
QY 282 DGGQSENQKPLFIL-----EDGASLKNVTMGDDGADG 313  
Db 974 DGGTSDGNPFAITSGGGRGGGVGQGGSVAGDADG 1012

## RESULT 15

US-10-282-122A-64726  
Sequence 64726, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl

APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 64726  
LENGTH: 694  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-10-282-122A-64726  
Query Match 8.4%; Score 193; DB 15; Length 694;  
Best Local Similarity 25.4%; Pred. No. 7.5e-05;  
Matches 86; Conservative 28; Mismatches 140; Indels 84; Gaps 14;  
QY 18 QSGDNGLGGH--NANSALGQOPIDROTIEQMAQLLAELLSLSPSGNNAATGAGNDQT 76  
Db 256 QTGGDGTGGHGTACTPTGTGDCAT-----ATAGSKATCGAGDGT 300  
QY 77 TGVGNAGLNGRKGKTAGTTQSDSQNMLSEWNGNGLDQAITPDGQGGQIGNPLLKAML 136  
Db 301 AAAGGGGNGDGGVA-----QGDIAAFGGDGNNGSDGVAAGSGGSGGAGG--AFV 352  
QY 137 KLIARMMDQSDQDFGQPGTGNNSASGT--SSGSGSPFNDLSGCK--APSGNSPSGNSPV 193  
Db 353 HIATATSTGGSGFG--GNGAASASGADGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410  
QY 194 STFSPPTPTSPSPLDPPSPSTKAAGSTPVT--DHPDP-----VGSAG 236  
Db 411 GG-----DGATGPGSGSGGNAGIARFDSDPPEAEPDVVGKGGGKGGSGG 456  
QY 237 IGAGNSVAFPSAGANQTVLHDTITVKAGQVFDGKQFTTAGSELGDDGSGSENQKPLFILE 296  
Db 457 LGVGGAGGTGGAGNG-----GAGGLLFGNGN---GGNAGAG-----D 493  
QY 297 DGASLKNVTMGDDGADGHLHYGDAKIDNL-HVTNVED 333  
Db 494 GGAGVAGGNGGCGGTATTTHEDPVAGVAVGVGGG 531

Search completed: January 25, 2005, 16:22:03  
Job time : 151 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 15:51:17 ; Search time 41 Seconds  
(without alignments)  
1048.997 Million cell updates/sec

Title: US-09-879-248-6  
Perfect score: 2310  
Sequence: 1 MSILTLNNTSSPGLFQSG.....LGDVENHYKVPMSANLKVAE 447  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2310	100.0	447	T18447	HrpW protein - Erw
2	353.5	15.3	221	A70045	pectate lyase homo
3	233.5	10.1	219	S68364	pectate lyase (EC
4	207	9.0	1660	A70869	hypothetical glyci
5	199.5	8.6	1306	A70934	hypothetical glyci
6	193	8.4	694	F70868	hypothetical glyci
7	188	8.1	639	D70931	hypothetical glyci
8	186.5	8.1	591	D70523	hypothetical glyci
9	186	8.1	1329	E70917	hypothetical glyci
10	185.5	8.0	1381	E70806	hypothetical glyci
11	185.5	8.0	1489	D70807	hypothetical glyci
12	183.5	7.9	242	A45724	pectate lyase (EC
13	183	7.9	588	F70971	hypothetical glyci
14	182	7.9	606	F70816	hypothetical glyci
15	182	7.9	731	C70974	hypothetical glyci
16	181.5	7.9	484	G70846	hypothetical glyci
17	180.5	7.8	1079	B70807	hypothetical glyci
18	179	7.7	730	F96559	hypothetical prote
19	179	7.7	1538	H70846	hypothetical glyci
20	179	7.7	3016	S77300	hypothetical prote
21	178	7.7	741	G70917	hypothetical glyci
22	177.5	7.7	1501	F70806	hypothetical glyci
23	177.5	7.7	2232	T34434	hypothetical prote
24	176.5	7.6	562	B70953	hypothetical glyci
25	175	7.6	645	F70825	probable ppe prote
26	174	7.5	615	H70589	hypothetical glyci
27	172.5	7.5	584	G70804	hypothetical glyci
28	172	7.4	3507	T34513	hypothetical prote
29	171.5	7.4	667	A70893	hypothetical glyci

ALIGNMENTS

RESULT 1

T18447  
HrpW protein - Erwinia amylovora  
C:Species: Erwinia amylovora  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18447  
R:Gaudriault, S  
submitted to the EMBL Data Library, May 1998  
A:Reference number: Z18936  
A:Accession: T18447  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-447 <GAU>  
A:Cross-references: UNIPROT:O54508; EMBL:Y13831; NID:e1293450; PID:e1293451; PIDN:CAA741  
A:Experimental source: strain CFBP1430; specific host Pomoideae  
C:Genetics:  
A>Note: hrpW

Query Match	100.0%	Score 2310;	DB 2;	Length 447;
Best Local Similarity	100.0%	Pred. No. 3.3e-119;	Mismatches 0;	Indels 0;
Matches 447;	Conservative 0;			Gaps 0;
QY	1	MSILTLNNTSSPGLFQSGDNGLGHNANSALGQQPIDRQTIIEQMAQLLAELLS	60	
Db	1	MSILTLNNTSSPGLFQSGDNGLGHNANSALGQQPIDRQTIIEQMAQLLAELLS	60	
QY	61	POSGNAATGAGNDQTTGVGNAGLNGRKGTTAGTTTQSDSQNMLSEMGNGLDQAITPDG	120	
Db	61	POSGNAATGAGNDQTTGVGNAGLNGRKGTTAGTTTQSDSQNMLSEMGNGLDQAITPDG	120	
QY	121	QGGGQIGDNPILLKMLIARMDGSDQFGQPGTGNNSASSGTSSTSSGSPNDLSGGKA	180	
Db	121	QGGGQIGDNPILLKMLIARMDGSDQFGQPGTGNNSASSGTSSTSSGSPNDLSGGKA	180	
QY	181	PSGNSPSGNYSPVSTFSPSTPTSPDLPFSSPTKAAGSTPVTDPDVGSAIGAG	240	
Db	181	PSGNSPSGNYSPVSTFSPSTPTSPDLPFSSPTKAAGSTPVTDPDVGSAIGAG	240	
QY	241	NSVAPTSAGANQTVLHDTITVKGQVFDGKGTFTAGSELGGQSGENQKPLFILEDGAS	300	
Db	241	NSVAPTSAGANQTVLHDTITVKGQVFDGKGTFTAGSELGGQSGENQKPLFILEDGAS	300	
QY	301	LKNVTMGDDGADGHIHYGDAKIDNLHVTNVGDAITVKNPSAGKSHVEITNNSPEHSD	360	
Db	301	LKNVTMGDDGADGHIHYGDAKIDNLHVTNVGDAITVKNPSAGKSHVEITNNSPEHSD	360	
QY	361	KILQLNADTNLSVDNVKADFGTFTVRTNGGQGNWDLNLSHISAEDGKFSFYKSDSEGLN	420	
Db	361	KILQLNADTNLSVDNVKADFGTFTVRTNGGQGNWDLNLSHISAEDGKFSFYKSDSEGLN	420	
QY	421	VNTSDISLGDVENHYKVPMSANLKVAE	447	

probable nucleopor  
hypothetical glyci  
hypothetical glyci  
hypothetical glyci  
circumsporozote p  
hypothetical glyci  
hypothetical glyci  
hypothetical glyci  
hypothetical glyci  
hypothetical glyci  
hypothetical prote  
Popai protein - Ps  
iron-regulated pro  
hypothetical glyci  
nuclear pore compl

Db 421 VNTSDISLGDVENHYKVPMSANLKVAE 447

RESULT 2  
A70045  
pectate lyase homolog yvpa - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: A70045  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallen  
ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: A70045  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-221 <KUN>  
A:Cross-references: UNIPROT:Q34310; GB:Z99121; GB:AL009126; NID:92635827; PIDN:CA815500.  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yvpa

Query Match 15.3%; Score 353.5; DB 2; Length 221;  
Best Local Similarity 41.8%; Pred. No. 1e-12;  
Matches 76; Conservative 31; Mismatches 70; Indels 5; Gaps 1;  
Db 250 ANQTVLHDTITVYKAGQVDFKGTFTAGSELGDSQENQKPLFILEDCASLKNVTMGDD 309  
27 AADKVHETIIIVKNTYDQKQRFVAGKELGDSQENQDPVFRVEDGATLKNVVLGAP 86  
310 GADGHIHYGDAKIDNLHVTNVEDATITVKNPSAGKSHVEITNSPFEHASKILOLNADT 369  
87 AADGVHTYGNVNIQNVKVEDGEDALTVK----KEGKVTIDGSAQKASDKIFQINKAS 141  
370 NLSVDNVKAKDFGTFRVNGGQGWDLNLSHSAEDGKFSFKSDSEGLNVTSDISLG 429  
142 TPTVKNFTADNGGKFIRQLGSGTFPHVDVIIDKCTITNMKEAIFRTDSTKSTVTRMTNTRY 201  
430 DV 431  
202 NV 203

RESULT 3  
S68364  
pectate lyase (EC 4.2.2.2) C - fungus (Fusarium solani)  
C:Species: Fusarium solani  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S68364  
R:Guo, W.; Gonzalez-Candelas, L.; Kolattukudy, P.E.  
Arch. Biochem. Biophys. 323, 352-360, 1995  
A:Title: Cloning of a new pectate lyase gene pelC from Fusarium solani f. sp. pisi (Nect  
A:Reference number: S68364; MUID:96063610; PMID:7487098  
A:Accession: S68364  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <GUO>  
A:Cross-references: UNIPROT:Q00843; EMBL:U13049  
C:Genetics:  
A:Gene: pelC  
A:Introns: 52/1; 102/3

C:Keywords: carbon-oxygen lyase

Query Match 10.1%; Score 233.5; DB 2; Length 219;  
Best Local Similarity 30.1%; Pred. No. 3.6e-06;  
Matches 63; Conservative 39; Mismatches 72; Indels 35; Gaps 6;  
QY 220 GGSTPTVTDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVYKAGQVDFKGTFTAGSE 279  
Db 8 GGVPKPTDH-----ISNS-----KVIEVKAGQVYDKWAKYDRSGG 43  
QY 280 LGDG-GQSENQKPLFILEDGLASLKNVTMGDDGADGHIHYGDAKIDNLHVTNVEGDAITVK 338  
Db 44 ACKQNEGGDDAIVFLLEGATLKNVITCKQSEGVHCKGHTLEFVWFEDVCEDAISIK 103  
QY 339 PNASGKSHVEITNSPFEHASKILOLNADTNLSVDNVKAKDFGTFTVNT--NGGQGNWD 396  
Db 104 EDKAKESW--IIGGAYHSDKVVQHNCGCTVNIINFVEDYGLKYRSCGNCCKQCKRN 161  
QY 397 LNLSHISAEDGKFSFKSDSEGLNVTSD 425  
Db 162 VVIEGVTTAKG-----GELAGINANYGD 184

RESULT 4  
A70869  
hypothetical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A70869  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: A70869  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1660 <COL>  
A:Cross-references: UNIPROT:O53215; GB:AL021246; GB:AL123456; NID:g3261507; PIDN:CAA1606  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv2490c  
C:Superfamily: collagen alpha 1(IV) chain

Query Match 9.0%; Score 207; DB 2; Length 1660;  
Best Local Similarity 28.1%; Pred. No. 0.0012;  
Matches 91; Conservative 19; Mismatches 130; Indels 84; Gaps 15;  
QY 7 NNNTSSPGLFQSGDNGLGGHNANSALGQQPIDRQTIEQMAQLLAELKSLSP--QSG 64  
Db 476 NGGAGNGGLV---GDGGAGGGGGAAG-----AGYADMTAIFLGSSGTPEGDGG 523  
QY 65 N----AATGAGG-NDQTTGVNAGLNGRKGTTAGTTPQSDSQNMLSEMGNGLDQA--IT 117  
Db 524 NGGAGGAGGAGGAHAGDGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 583  
QY 118 PDGCGGGQIGDNPILKMLKLIRMMWDGSDQFGQGTGNNSSASGCTSSSGG---SPFND 174  
Db 584 GDGGAGGAGGDDPAGRA-----GSQGVGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633  
QY 175 LSGGKAPSGNSP-SGNYSPVSTFPSTPTSTPSLDPFSPSTKAGGSPVTPVTHDPVPG 233  
Db 634 GDGGAGGDDGDPGAGKGGAG-----GAGATEGVTGATGATVHSG--G 674  
QY 234 SAGIGAGNSVAFTSAGANQTVLHDTITVYKAGQVDFKGTFTAGSELGDSQENQKPLF 293  
Db 675 NGGKG-GNGADATVAGN-----GKGGAGNGGLVGGGAG----- 710  
QY 294 ILEDG----ASLKNVTMGDDGADG 313  
Db 711 --GDGSGNAGANGANVGEDGADG 732



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A/Gene: kv2487C
C/Superfamily: uncharacterized glycine-rich protein, PE motif containing

Query Match      8.4%; Score 193; DB 2; Length 694;
Best Local Similarity 25.4%; Pred. No. 0.0024;
Matches 86; Conservative 28; Mismatches 140; Indels 84; Gaps 14

Qy   18 QSGEDNGLGHH-NANSALGOOPTIDRQTIEWAQLLAELLKSLSPQSQNATGAGCNDOOT 76
    :|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   256 QTGGDGGTGHGTAGTTGGTGGDGAT-----ATAGSKATGGAGGDGT 300

Qy   77 TGVNAGLNGRKCTACTTPQSDSQNNMLSEMGNNGLDQAITPDGGGGQIGDNPLLKAWL 136
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   301 AAGGGGGNGDGGVA---QGITASAFGGDGGNSDGVAAAGSGSGGAGGG----AFV 352

Qy   137 KLIAARMDDGQSDQFGPGTGNNSSASTP-SSSGGSPFNLDLSGGK--APSGNSPSGNYSVPV 193
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   353 HIATATSTGSGGFG--GNGAASAASADGGAGGAGNGGAGGLLPFGDGGNGGAGGAGGI 410

Qy   194 STFSPPSTPTSPFLDFPASPTKVAAGSTPVTV--DHDPD-----VGSAQ 236
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   411 GG-----DGAETGGPGSGSNGAGIARFDSFDPEABPDVVGGKGDDGKGKGGSG 456
```

[illegible]

RESULT 7  
D70931  
hypothetical glycine-rich protein Rv1803c - Mycobacterium tuberculosis (strain  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Mar-2003  
C:Accession: D70931  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;  
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho-  
Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A: Authors: Sgares, R.; Sulstony, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the comple-  
A: Reference number: A70500; MUID: 98295987; PMID: 9634230  
A: Accession: D70931  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-639 <COL>  
A: Cross-references: GB:AL022021; GB:AL123456; NID:G3250699; PIDN:CAA17724.1; P:  
A: Experimental source: strain H37Rv

[illegible]



Query Match 8.0%; Score 185.5; DB 2; Length 1381;  
Best Local Similarity 25.0%; Pred. No. 0.014;  
Matches 79; Conservative 25; Mismatches 141; Indels 71; Gaps 11;

QY 19 SGDDNGLGCHNANSALGQC--PIDRTQIBQMAQLLAELKSLSPSGNAATGAGNDQT 76  
DB 779 SGDDGKGQGGSGGTGSGAPI-----GGAGGTGSGGH 814

QY 77 TGVGNAGLNKRGTAGTTTQSDSQNMLSEMNGNLDQAITPDGQG--QIQDNPLLKAM 135  
DB 815 AKGGGAGGI-GAQCQTITTVPGNGN--AGDGGNGNAGA---GNGGSGDFGNT----- 863

QY 136 LKLIARMMDQSDQDQCPGTGNNSASSGTSSGGSPFNDLGGKAPS--GNSPSGNYSPVS 194  
DB 864 -----TSGASGSGGNGNAGTAGSGAGGTGTGLSGGNGGNGGNGGDDGGNG 913

QY 195 TFSPPSTPTSPSPIDFPSPPTKAAGGSPVTDHPDVPVGSAGIGAGNSVAFTSAGANQTV 254  
DB 914 AHGTGVAQVPAISLPTFNGGAGGNGTSGNGAGPAGAPGPTTGGNAGSGGIGDGGN 973

QY 255 LHDTITVKAQVFDG-----KQQTFTAGS-----ELGDDGQSENOKPLFILED 297  
DB 974 GGD-----CGKGGDGAADVNVFMPTEPQAATGTAGSAGDPTGNGGPGTGPSPVWAPP 1028

QY 298 GASLKNVTMGDDGADG 313  
DB 1029 PTPITQVQQGGDGGAG 1044

RESULT 11  
D70807  
hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: D70807  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70807  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1489 <COL>  
A:Cross-references: GB:AL022022; GB:AL123456; NID:93261554; PIDN:CAA17751.1; PID:g292445  
A:Experimental source: strain H37RV  
C:Genetics:  
C:Superfamily: collagen alpha 1(IV) chain

Query Match 8.0%; Score 185.5; DB 2; Length 1489;  
Best Local Similarity 23.9%; Pred. No. 0.015;  
Matches 85; Conservative 26; Mismatches 136; Indels 109; Gaps 12;

QY 10 TSSSPCLFOSGDNGLGCHNANSALGQCQPIDRTQIBQMAQLLAELKSLSPSGNAATG 69  
DB 726 TTGNAGVGGAGSSGAGTNGSGAGG-----TDQGGAGGAG 763

QY 70 AGNDQTTGVG-----NAGLNGRKGTAGTTTQSDSQNMLSEMNGNLDQAIT 117  
DB 764 GAGADNPTGIGTGGDGTGGAAGAGGAGGAGTGT-----GGMIGTTGNAGV----- 812

QY 118 PQGGGGQIGDNPLLKAM.LIARMDGQSDQDQCPG-TGNNSASGTSSSGSPNDLS 176  
DB 813 --CGAGGQGGDGG-----AGGAGADADQPGTGTGTFAGGAGGAGGSGSSCA 858

QY 177 GKGAPSGNSPSGNYSPVSTPSTPTSPIDFPSPPTKAAGGSPVTDHPDVPVGSAG 236  
DB 859 GGTNGSGGA-GGTCCGV-----VAGGAGISFNSNGSGTGGTGGTGGDGGNAG 908

QY 237 TGA-----GNSVAFTSAGAN-----QTVLHDTITVKAG 264  
DB 909 TGAGDPKPGTGTGTGGTGGGAGGCGGANFNGTGTGTGGKGLNLTGLSSATSGTG 968

QY 265 QV--PDGKGQTFTAGSEL-----GDGQSENOKPLFILEDGASLKNVTMGDDGADG 313  
DB 969 GTGGTGGKGTGGAGDSDSAGGTGGTGGAGGAGAGLANTGCTAGNAGIGDGGQG 1024

RESULT 12  
A45724  
pectate lyase (EC 4.2.2.2) - fungus (Fusarium solani)  
C:Species: Fusarium solani  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45724  
R:Gonzalez-Candelas, L.; Kolattukudy, P.E.  
J. Bacteriol. 174, 6343-6349, 1992  
A:Title: Isolation and analysis of a novel inducible pectate lyase gene from the phytop  
A:Reference number: A45724; MUID:93015682; PMID:1400187  
A:Accession: A45724  
A>Status: preliminary  
A:Molecule type: DNA; protein  
A:Residues: 1-242 <GON>  
A:Cross-references: UNIPROT:Q04701; GB:M94691; NID:gl168155; PIDN:AAA33338.1; PID:gl16815  
A:Experimental source: isolate T8  
A:Note: sequence extracted from NCBI backbone (NCBIN:115473, NCBIIP:115474)  
C:Keywords: carbon-oxygen lyase

Query Match 7.9%; Score 183.5; DB 2; Length 242;  
Best Local Similarity 30.5%; Pred. No. 0.0022;  
Matches 62; Conservative 32; Mismatches 80; Indels 29; Gaps 8;

QY 235 AGIGAGNSVAFT-----SAGANQTVLHDTITVKAQVFDGKGTFTAGSELGDDGQSENQ 289  
DB 9 AALVCTSSAAVTKTLPKSAGA--TSFPTAVPVKGS--YDGMKRFEREPEKVKGDDETGE 64

QY 290 K-PLFILEDGASLKNVTMGDDGADGIHLGDAKIDNLHVTNVGEDIAITVKPSAGKSHV 348  
DB 65 KDAMFILENGATLSNVIIGASQAEVHCCKGTCTLNVMWADVCEDAVTLKQTSCTS----- 120

QY 349 EITNSSFFHASDKILQLNADTNLSVDNKAQDFGTFVFT-----NGGQGNWDLNLSH 402  
DB 121 YINGGGAFAHSDKILQFNGRGTIVHVDFYADYGLKRSCKNGKNGGPR---NVIVENS 177

QY 403 SAEDKGFSFKVSDSEGLNVNTSD 425  
DB 178 VAVDGGVLC-----GINTNYGD 194

RESULT 13  
F70971  
hypothetical glycine-rich protein Rv3367 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Mar-2003  
C:Accession: F70971  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70971  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-588 <COL>  
A:Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA15752.1; PID:ei12022  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv3367  
C:Superfamily: uncharacterized glycine-rich protein, PE motif containing

Query Match 7.9%; Score 183; DB 2; Length 588;

Best Local Similarity 23.1%; Pred. No. 0.0068; Matches 83; Conservative 20; Mismatches 151; Indels 106; Gaps 11;	
QY 7 NNNTSSPGLFOSGDNGLGCHN-----ANSALGQOPIDRQTIEQMAQL 50	
DB 208 NCGAGGAAGLGGSGGGGGGGLTGNDCGNPAPVTNPALNAGAGDSNIEPQT-----260	
QY 51 LAELLKSLSPSGNAATG-----AGNDQTTGVGNA-----GGL 85	
DB 261 -----SVLIGTGGDTGGAGVNGGNGGAGGDANGNPANTSINAGAGGNGAAGDGA 315	
QY 86 NGRKGTAGTTPQSDSQNMLSEMNGNLDOAITPDGQGG-----GOIGDNPLLKAMLKLIAR 141	
DB 316 NCGAGGAGGQAASAGSSVGGDGGNGAGGTGTNGHAGGAGGAGGAGGR-----GG 365	
QY 142 MWDGSDQDQPGTGNNSASSGTSSSCGSPFNDLGGKAPSGNSPNSVSTSPSPST 201	
DB 366 WLVGNGGNGGNGAAGNGAIGGTGGAGGVPAN--CGNSALGTQPVGG-----DGGDGGNG 419	
QY 202 PTPSPFLPFPSPPTKAAG-----GSTPVTDPDPVGSAGTGAAGNSVAFTSAGANQTVL 255	
DB 420 GTGTGGRGDDGSGGAGASWLMNGNGNGGNGGTGGSGGVGGNGGIGDAGGNGATS 479	
QY 256 HDITITVKAQVDFGKGQTFTAGSELGDSQSENQKPLFILEDCASLKNVTMGDDGADGIH 315	
DB 480 TSSIP-----FDAHGNGGAGGDAGHGG-----TGDDGGDGGH 512	
RESULT 14	
H70816	
hypothetical glycine-rich protein Rv0872c - Mycobacterium tuberculosis (strain H37RV)	
C:Species: Mycobacterium tuberculosis	
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003	
C:Accession: H70816	
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998	
A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	
A: Reference number: A70500; MUID:98295987; PMID:9634230	
A: Accession: H70816	
A: Status: preliminary; nucleic acid sequence not shown; translation not shown	
A: Molecule type: DNA	
A: Residues: 1-606 <COL>	
A: Cross-references: GB:AL022004; GB:AL123456; NID:G3261550; PIDN:CAA17678.1; PID:el25401	
A: Experimental source: strain H37RV	
C: Genetics:	
C: Superfamily: uncharacterized glycine-rich protein, PE motif containing	
Query Match 7.9%; Score 182; DB 2; Length 606;	
Best Local Similarity 26.4%; Pred. No. 0.008;	
Matches 90; Conservative 27; Mismatches 112; Indels 112; Gaps 15;	
QY 16 LFQSGDNGLGHNANSALGQOPIDRQTIEQMAQLLAELLKSLSPSGNAATGAGNDQ 75	
DB 220 LFGSGAGGQGGNGAAGGVNP-----TPTGTADAGSTGTQ 257	
QY 76 TTGVGNAGLNGRKGTAGTTPQSDSQNMLSEMNGNLDOAITPDGQGG-GGQIGDNPLLKA 134	
DB 258 TLG-GNAIGNGGPGDAGDAMTSGG-----AGSGGNAVSTVNGDVGGBEGKG-----305	
QY 135 MLKLIARMMDGSDQDQPGTGNNSASSGTSSSGSPFNDLGGKAPS-----GNSPSGN 189	
DB 306 -----GEGAYGAGGAGGSAASIGNAIFGG---NGGAGGNAQAPGGVGGAGGEG 352	
QY 190 YSPVSTFPSPSTPT-----SPTPLD-FPSSPTKAAGS-----222	
DB 353 DAQVGTNSFNAEAGNCGSGGNGFDSFASGTCGAGTGGAGRGGLLICDGGAGGAGV 412	
QY 223 --TPVTDPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVKAQVDFDKG-----QT 273	

Db 413 GQTGSGAPGGGGGAG-GDGAANTDSAGSSR-----KAPGGDGGVGGDGASA 459	
QY 274 FTAGSELGDSQSENQKPLFILEDCASLKNVTMGDDGADGI 314	
DB 460 LQTGGEGIGGGGN-----GGAG--GLLIGNGGAGGV 490	
RESULT 15	
C70974	
hypothetical glycine-rich protein Rv3388 - Mycobacterium tuberculosis (strain H37RV)	
C:Species: Mycobacterium tuberculosis	
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003	
C:Accession: C70974	
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998	
A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	
A: Reference number: A70500; MUID:98295987; PMID:9634230	
A: Accession: C70974	
A: Status: preliminary; nucleic acid sequence not shown; translation not shown	
A: Molecule type: DNA	
A: Residues: 1-731 <COL>	
A: Cross-references: GB:AL009198; GB:AL123456; NID:G3242262; PIDN:CAA15773.1; PID:G266166	
A: Experimental source: strain H37RV	
C: Genetics:	
A: Gene: Rv3388	
C: Superfamily: elastin related uncharacterized glycine-rich protein, PE motif containing	
Query Match 7.9%; Score 182; DB 2; Length 731;	
Best Local Similarity 25.3%; Pred. No. 0.01;	
Matches 89; Conservative 26; Mismatches 127; Indels 110; Gaps 15;	
QY 7 NNNTSSPGLFOSGDNGLGHNANSALGQOPIDRQTIEQMAQLLAELLKSLSPSGNA 66	
DB 399 NNTSAGTGGVGASGSGTGNAG-----LIGAGGHGG 428	
QY 67 ATGAGNDQTTGVGNAGLNGRKGTAGTTPQ-----SDSQN---MLSEMNGNLDOAIT 117	
DB 429 AGGAGCN-QTGGVGN-GGAGNGGAGGAGGQLYNGVGGDGGNGGAGGANIAGNGSDGNA 486	
QY 118 PDQGGGGIGDNPLLKAMLKLIARMMDGSDQDQPGTGNNSAS-----SQTSSSGSP 171	
DB 487 GHGGAGGS-----ARLI-GAGGHGGDGGAGGNTAGRRADAIAGTGGDGGNG 531	
QY 172 FNDLSGGKAPSGNSPNSVSTPSTPTSPSPDFFSSPTKAAGSTPVTIDHDP 231	
DB 532 GN-----GGLLSGNAGAGHGGAGGSGSTATTG-----TPPTGATGNN-----570	
QY 232 VGSAGIGAGNSVAFTSAGANQTVLHDTITVKAQVDFDKGQFTTAGSELGDSQSENQKP 291	
DB 571 -GGNG-GAGGTAGTGG-----GIGNGGAGGTGCGNAGV-----604	
QY 292 LFILEBDGASLKNVTMGDDCADGIHLYGDAKIDNLHVTNVGDEAITVKPNSAG 343	
DB 605 LSVGSGTGLGGNGSGGLGGGGSLFGNGGAGGVGATG-GNGSGSIGPASVG 655	

Search completed: January 25, 2005, 16:10:17  
Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 15:23:52 ; Search time 198 Seconds  
(without alignments)  
1298.952 Million cell updates/sec

Title: US-09-879-248-6  
Perfect score: 2310  
Sequence: 1 MSILTLNNTSSPGLFQSG.....LGDVENHYKVPMSANLKVAE 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2310	100.0	447	054508	O54508 erwinia amy
2	2277	98.6	447	Q9LAW2	Q9LAW2 erwinia amy
3	1916.5	83.0	450	Q6XDB8	Q6XDB8 erwinia pyr
4	1916.5	83.0	450	AAQ17046	AAQ17046 erwinia p
5	1916.5	83.0	450	AA545453	AA545453 erwinia p
6	1005	43.5	479	Q6RK52	Q6RK52 pectobacter
7	1005	43.5	479	Q6D5C8	Q6D5C8 erwinia car
8	1005	43.5	479	AA520352	AA520352 pectobact
9	705	30.5	138	Q79AW7	Q79AW7 erwinia amy
10	589	25.5	424	Q8RP12	Q8RP12 pseudomonas
11	567.5	24.6	441	Q87327	Q87327 pseudomonas
12	559	24.2	424	Q87264	Q87264 pseudomonas
13	559	24.2	424	Q7C415	Q7C415 pseudomonas
14	472.5	20.5	386	Q849P3	Q849P3 pseudomonas
15	423.5	18.3	307	Q8KKZ2	Q8KKZ2 rhizobium e
16	415.5	18.0	380	Q8XVQ5	Q8XVQ5 raletonia s
17	362.5	15.7	224	Q9RHW0	Q9RHW0 bacillus sp
18	354	15.3	203	Q8PIH5	Q8PIH5 xanthomonas
19	353.5	15.3	221	Q34310	Q34310 bacillus su
20	349.5	15.1	222	Q9X6Z2	Q9X6Z2 bacillus sp
21	346.5	15.0	324	Q8PBA4	Q8PBA4 xanthomonas
22	341	14.8	222	Q8LOR5	Q8LOR5 bacillus sp
23	256	11.1	276	Q829M8	Q829M8 streptomyce
24	226.5	9.8	266	Q9EX16	Q9EX16 streptomyce
25	216.5	9.4	215	Q00843	Q00843 nectria hae
26	207	9.0	1660	Q79FD4	Q79FD4 mycobacteri
27	207	9.0	1660	CA555496	CA555496 mycobacte
28	207	9.0	1665	Q7D721	Q7D721 mycobacteri
29	206	8.9	252	Q7S4B7	Q7S4B7 neurospori
30	199.5	8.6	1306	Q7D9L6	Q7D9L6 mycobacteri
31	199.5	8.6	1306	Q7U1Q7	Q7U1Q7 mycobacteri

32 199.5 8.6 1306 2 Q6MX28  
33 199.5 8.6 1306 2 CA55300  
34 194.5 8.4 233 2 Q00845  
35 194 8.4 1928 2 Q8T9H1  
36 193 8.4 240 2 Q93877  
37 193 8.4 694 2 Q7D724  
38 193 8.4 694 2 CA55495  
39 191 8.3 555 2 Q8SX80  
40 191 8.3 929 2 Q9NBL3  
41 191 8.3 929 2 Q9NBW0  
42 191 8.3 929 2 AAS64813  
43 191 8.3 939 2 Q7KRH9  
44 191 8.3 939 2 Q9NHQ0  
45 191 8.3 939 2 AAS64812

## ALIGNMENTS

RESULT 1  
O54508 PRELIMINARY; PRT; 447 AA.  
AC O54508;  
DT 01-JUN-1998 (TREMELrel. 06, Created)  
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE HrpW protein.  
GN Name=hrpW;  
OS Erwinia amylovora  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OC NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CFBP1430;  
RX MEDLINE=98086111; PubMed=9426142;  
RA Gaudriault S., Malandrin L., Paulin J.P., Barny M.A.;  
RT "DspA, an essential pathogenicity factor of Erwinia amylovora showing  
RT homology with AvrE of Pseudomonas syringae, is secreted via the Hrp  
RT secretion pathway in a DspB-dependent way.";  
RL Mol. Microbiol. 26:1057-1069(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CFBP1430;  
RX MEDLINE=98316710; PubMed=9654138;  
RA Gaudriault S., Brisset M.N., Barny M.A.;  
RT "HrpW of Erwinia amylovora, a new Hrp-secreted protein.";  
RL FEBS Lett. 428:224-228(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ea321;  
RA Kim J.F., Zumboff C.H., Beer S.V.;  
RT "HrpW, a new harpin of Erwinia amylovora, is a member of a family of  
RT pectate lyases.";  
RL Phytopathology 87:0-0(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ea321;  
RX MEDLINE=98422475; PubMed=9748455;  
RA Kim J.F., Beer S.V.;  
RT "HrpW of Erwinia amylovora, a new harpin that contains a domain  
RT homologous to pectate lyases of a distinct class.";  
RL J. Bacteriol. 180:5203-5210(1998).  
DR EMBL; Y13831; CAA74158.1; -;  
DR EMBL; U94513; AAC62314.1; -;  
DR FIR; T18447; T18447.  
DR HSSP; Q9RHW0; 1EB6.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0030570; F:pectate lyase activity; IEA.  
DR InterPro; IPR011050; Pectin\_lyas\_like.  
DR InterPro; IPR004898; Pect\_lyase.  
DR Pfam; PF03211; Pectate\_lyase; 1.  
SQ SEQUENCE 447 AA; 45347 MW; 7A744D169D6D9CF3 CRC64;

Query Match		100.0%;	Score 2310;	DB 2;	Length 447;	
Best Local Similarity		100.0%;	Pred. No. 2.3e-110;			
Matches 447;		Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQGPIDRQTIEQMAQLLAELLKSLLS	60			
Db	1	MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQGPIDRQTIEQMAQLLAELLKSLLS	60			
Qy	61	POSGNAATGAGNDQTTGAGNAGGLNGRKGTTAGTTTQSDSQNMLSEMNGNGLDQAITPDG	120			
Db	61	POSGNAATGAGNDQTTGAGNAGGLNGRKGTTAGTTTQSDSQNMLSEMNGNGLDQAITPDG	120			
Qy	121	QGGQIGDNPLKAMKLIARMDGQSDQFQPGTGNNSASCTSSSGSPFNDSGGKA	180			
Db	121	QGGQIGDNPLKAMKLIARMDGQSDQFQPGTGNNSASCTSSSGSPFNDSGGKA	180			
Qy	181	PSGNSPBGNSPVSTFSPSTPTSPDPPSSPTKAAGGTPVTDHPDPVGSAGIGAG	240			
Db	181	PSGNSPBGNSPVSTFSPSTPTSPDPPSSPTKAAGGTPVTDHPDPVGSAGIGAG	240			
Qy	241	NSVAFTSAGANQTVLHDTITVRAGQVFDGKGTFTAGSELGSGQSENQKPLFILEDGAS	300			
Db	241	NSVAFTSAGANQTVLHDTITVRAGQVFDGKGTFTAGSELGSGQSENQKPLFILEDGAS	300			
Qy	301	LKNVTMGDDGADGHIHYGDAKIDNLHVTNVGDAITVKPNSAGKSHVEITNSSFEHSD	360			
Db	301	LKNVTMGDDGADGHIHYGDAKIDNLHVTNVGDAITVKPNSAGKSHVEITNSSFEHSD	360			
Qy	361	KILOLNADTNLSVDNVKAKDFGTFRVTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN	420			
Db	361	KILOLNADTNLSVDNVKAKDFGTFRVTNGGQGNWDLNLSHISAEDGKFSFKVSDSEGLN	420			
Qy	421	VNTSDISLSDVENHYKVPMSANLKVAE	447			
Db	421	VNTSDISLSDVENHYKVPMSANLKVAE	447			
RESULT 3						
Q6XDB8		PRELIMINARY;	PRT;	450	AA.	
AC	Q6XDB8;					
DT	05-JUL-2004	(Tremblrel. 27, Created)				
DT	05-JUL-2004	(Tremblrel. 27, Last sequence update)				
DT	05-JUL-2004	(Tremblrel. 27, Last annotation update)				
DE	hrpw.					
GN	Name=hrpw;					
OS	Erwinia pyrifoliae.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Erwinia.					
OX	NCBI_TaxID=79967;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=WT3;					
RA	Shrestha R., Baek S.J., Bae H.N., Cho J.M., Park D.H., Hwang I.K.,					
RA	Hur J.H., Lim C.K.;					
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=WT3;					
RA	Shrestha R., Baek S.J., Park D.H., Bae H.N., Cho J.M., Hwang I.,					
RA	Hur J.H., Lim C.K.;					
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AY237642; AAO17046.1; -					
DR	EMBL; AY530755; AAS45453.1; -					
DR	InterPro; IPR011050; Pectin_lyas_like.					
DR	InterPro; IPR004898; Pect_lyase.					
DR	Pfam; PF03211; Pectate lyase; 1.					
SQ	SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;					
Query Match						
Best Local Similarity		83.0%;	Score 1916.5;	DB 2;	Length 450;	
Matches 376;		Conservative	23;	Mismatches 46;	Indels 7;	Gaps 2;
Qy	1	MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQGPIDRQTIEQMAQLLAELLKSLLS	60			
Db	1	MSVLTNLNISIPSSQGLFKPGEDNGLSQNTNSAQGQHPIDRQTIEQMAQLLAELLKPLLS	60			
Qy	61	POSGNAATGAGNDQTTGAGNAGGLNGRKGTTAGTTTQSDSQNMLSEMNGNGLDQAITPDG	120			
Db	61	POADNAA--AGSNDQTNVGNGAGGLTGQNGAAGTTTQSVNQTMLSEMNGNGLDQAITPDG	118			
RESULT 2						
Q9LAW2		PRELIMINARY;	PRT;	447	AA.	
AC	Q9LAW2;					
DT	01-OCT-2000	(Tremblrel. 15, Created)				
DT	01-OCT-2000	(Tremblrel. 15, Last sequence update)				
DT	01-JUN-2003	(Tremblrel. 24, Last annotation update)				
DE	Harpin HrpW.					
GN	Name=hrpw;					
OS	Erwinia amylovora.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Erwinia.					
OX	NCBI_TaxID=552;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Ea246;					
RA	Kim J.F., Laby R.J., Beer S.V.;					
RL	Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AF083620; AAF63402.1; -					
DR	HSP; Q99H0; IE66					
DR	GO; GO:000576; C:extracellular; IEA.					
DR	GO; GO:0030570; F:pectate lyase activity; IEA.					
DR	InterPro; IPR011050; Pectin_lyas_like.					
DR	InterPro; IPR004898; Pect_lyase.					
DR	Pfam; PF03211; Pectate lyase; 1.					
SQ	SEQUENCE 447 AA; 45340 MW; 0BBAAE3871EDC2F6 CRC64;					
Query Match						
Best Local Similarity		98.6%;	Score 2277;	DB 2;	Length 447;	
Matches 441;		Conservative	3;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQGPIDRQTIEQMAQLLAELLKSLLS	60			
Db	1	MSILTLNNNTSSPGLFQSGDNGLGHNANSALGQGPIDRQTIEQMAQLLAELLKSLLS	60			

QY 121 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGTGNNSASCTSSGGSPFNDLS --- 176  
 DB 119 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGSGNNDASSGSPSAGNYPASNASGSS 178  
 QY 177 -GGKAPSGNSPSGNYSPVSTFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGSA 235  
 DB 179 LGSSSLGKASSGGTSTNSFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGST 238  
 QY 236 GIGAGNSVAFSTAGANOTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 295  
 DB 239 GVGAGNSVGFSTAGANPTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 298  
 QY 296 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 355  
 DB 299 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 358  
 QY 356 EHASDKILOLNADTNLSVDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 415  
 DB 359 EHASDKILOLNADTNLTNDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 418  
 QY 416 SEGNNVNTSDISLGNVENHYKVPMSANLKVAE 447  
 DB 419 SEGNNVNTSDISLGNVENHYKVPMSANLKVAK 450

## RESULT 4

AAQ17046 PRELIMINARY; PRT; 450 AA.  
 ID AAQ17046;  
 AC AAQ17046;  
 DT 03-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 03-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 03-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE HRPW.  
 GN HRPW.  
 OS Erwinia pyrifoliae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 OX NCBI\_TaxID=79967;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WT#3;  
 RA Shreetha R., Baek S.J., Bae H.N., Cho J.M., Park D.H., Hwang I.K.,  
 RA Hur J.H., Lim C.K.;  
 RT "Molecular characterization hrp genes cluster of Erwinia pyrifoliae  
 RT and expression of hrpP encoding elicitor of the hypersensitive  
 RT response.";  
 RL Submitted (PEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY237642; AAQ17046.1; -  
 SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;

Query Match 83.0%; Score 1916.5; DB 2; Length 450;  
 Best Local Similarity 83.2%; Pred. No. 2.9e-90;  
 Matches 376; Conservative 23; Mismatches 46; Indels 7; Gaps 2;  
 QY 1 MSLLTINNTSSPGILFQSGDNGLGHHNANSALGQOPIDROTIEQMAQLLELLKSLLS 60  
 DB 1 MSVLTINISIPSSQGLFKPEDNGLSGQNTNSAQGHPIDROTIEQMAQLLELLKSLLS 60  
 QY 61 PQSGNAATGAGNDQTTGVNAGGLNGRGTAGTTTQSDSQNNLSBMGNNGLDQAITPDG 120  
 DB 61 PQADNAA--AGSNDQTNQVGNAGGLTGQGAAGTTTQSVNQTMLGEMNGNGLDQAITPDG 118  
 QY 121 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGTGNNSASCTSSGGSPFNDLS --- 176  
 DB 119 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGSGNNDASSGSPSAGNYPASNASGSS 178  
 QY 177 -GGKAPSGNSPSGNYSPVSTFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGSA 235  
 DB 179 LGSSSLGKASSGGTSTNSFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGST 238  
 QY 236 GIGAGNSVAFSTAGANOTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 295  
 DB 239 GVGAGNSVGFSTAGANPTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 298  
 QY 296 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 355  
 DB 299 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 358  
 QY 356 EHASDKILOLNADTNLSVDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 415  
 DB 359 EHASDKILOLNADTNLTNDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 418  
 QY 416 SEGNNVNTSDISLGNVENHYKVPMSANLKVAE 447  
 DB 419 SEGNNVNTSDISLGNVENHYKVPMSANLKVAK 450

QY 296 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 355  
 DB 299 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 358  
 QY 356 EHASDKILOLNADTNLSVDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 415  
 DB 359 EHASDKILOLNADTNLTNDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 418  
 QY 416 SEGNNVNTSDISLGNVENHYKVPMSANLKVAE 447  
 DB 419 SEGNNVNTSDISLGNVENHYKVPMSANLKVAK 450

## RESULT 5

AAS45453 PRELIMINARY; PRT; 450 AA.  
 ID AAS45453;  
 AC AAS45453;  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE HRPW.  
 GN HRPW.  
 OS Erwinia pyrifoliae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 OX NCBI\_TaxID=79967;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WT#3;  
 RA Shreetha R., Baek S.J., Park D.H., Bae H.N., Cho J.M., Hwang I.,  
 RA Hur J.H., Lim C.K.;  
 RT "Identification of hrp genes cluster and characterization of HR  
 RT elicitor hrpNep gene in Erwinia pyrifoliae.";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY530755; AAS45453.1; -  
 SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;

Query Match 83.0%; Score 1916.5; DB 2; Length 450;  
 Best Local Similarity 83.2%; Pred. No. 2.9e-90;  
 Matches 376; Conservative 23; Mismatches 46; Indels 7; Gaps 2;  
 QY 1 MSLLTINNTSSPGILFQSGDNGLGHHNANSALGQOPIDROTIEQMAQLLELLKSLLS 60  
 DB 1 MSVLTINISIPSSQGLFKPEDNGLSGQNTNSAQGHPIDROTIEQMAQLLELLKSLLS 60  
 QY 61 PQSGNAATGAGNDQTTGVNAGGLNGRGTAGTTTQSDSQNNLSBMGNNGLDQAITPDG 120  
 DB 61 PQADNAA--AGSNDQTNQVGNAGGLTGQGAAGTTTQSVNQTMLGEMNGNGLDQAITPDG 118  
 QY 121 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGTGNNSASCTSSGGSPFNDLS --- 176  
 DB 119 QGGQIGDNPPLKAMKLIARMDGSDQDQFGPGSGNNDASSGSPSAGNYPASNASGSS 178  
 QY 177 -GGKAPSGNSPSGNYSPVSTFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGSA 235  
 DB 179 LGSSSLGKASSGGTSTNSFSPSTPTSPSLDFFPSPTTAAAGSTPVTHDHPDVGST 238  
 QY 236 GIGAGNSVAFSTAGANOTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 295  
 DB 239 GVGAGNSVGFSTAGANPTVLHDTITVKGQVDFGKGTFTAGSELGGGSGENKPLFIL 298  
 QY 296 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 355  
 DB 299 EDGASLKNTVMGDDGADGHIHYGDAKIDNLHVTNVEDAITVKPNSAGKSHVITNSSP 358  
 QY 356 EHASDKILOLNADTNLSVDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 415  
 DB 359 EHASDKILOLNADTNLTNDNVKAKDFGTFRVTRNGGQGNWDLNLSHISAEDGKFSFVKSD 418  
 QY 416 SEGNNVNTSDISLGNVENHYKVPMSANLKVAE 447  
 DB 419 SEGNNVNTSDISLGNVENHYKVPMSANLKVAK 450



OS Erwinia carotovora subsp. atroseptica SRI1043.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=218491;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=SCRI1043;  
RA Bell K.S., Sebahia M., Pritchard L., Holden M., Hyman L.J.,  
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,  
RA Atkin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,  
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,  
RA Frimond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,  
RA Almond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;  
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL: BX950851; CAG75014.1;  
DR EMBL: BX950851; CAG75014.1;  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

Query Match 43.5%; Score 1005; DB 2; Length 479;

Best Local Similarity 49.9%; Pred. No. 1.1e-43;  
Matches 231; Conservative 60; Mismatches 102; Indels 70; Gaps 15;

Qy 8 NNTSSPGLFQSGDNGLGHNSALGQDPIDRQTIQMAQLLAELLSL----- 59  
Db 61 NTPSSTDG--SSQQAQI-GNGSSALGQN-----GSAADMLKLEALIPSKNGQEA 110  
Qy 60 -SPQSGNAATGAGN---DQTTGVNAGLNGRKGTTAGTTTQSDSQNMLSEMNGNLDQA 115  
Db 111 GNPLSSGSSGAAGNSGASPLTSGSGAGVGGAQ-----NPEDLSRLQDSAGSALNNA 165  
Qy 116 ITPDQGGGGIGDNPPLKMLKLIARMQDSQDFQPGTGNNSSASGTSSSGSGSPFNDL 175  
Db 166 INPTADGGGQLSGNDLLKALLELIGNLMDSQKGEFGQP-----QSGSQSGGSGP--- 215  
Qy 176 SGKAPSGNSPNSVSTFSPSTPTSPSLDFPSSPTKAAG-----STPVTDPD 230  
Db 216 STG-APQASSGGGGSPAA-----PSAPSSVGGNGGAAPLTAAPT 257  
Qy 231 PV--GSAG-----IGAGNSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGD 282  
Db 258 GVDGSAASPTASTAGAG-PVSPPTASANTVVDITIKVGFGEVFDGKGTFTAGSELGD 316  
Qy 283 GGQSENOKPLFIEDGASLKNVTMGDDGADGIHLGYDAKIDNLHVTNVGEDALTIVKPSA 342  
Db 317 GGQAGOKPLFELAQATLKNVFGDNDAGVHVRGDAKIDNVHVTNVGEDALTIVKPSN- 375  
Qy 343 GKSHVEITNSSEFHASDKILQNLADTNLSVDNVKADFGFTVTRNGGQGGNDLNLSHI 402  
Db 376 GKPAVEITNSAQAQSKIFQLNADANLTIDNFKAKDFGFTVTRNGGQGGNDLNLNSI 435  
Qy 403 SAEDGKFSVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKV 445  
Db 436 DAENGKFSVKSDSEGLNVKGNINLTNNVNNHYKVPDSANLQV 478

RESULT 8

AAS20352 PRELIMINARY; PRT; 479 AA.

ID AAS20352  
AC AAS20352;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE HRPW.  
GN HRPW.

OS Pectobacterium atrosepticum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=SCRI1039;  
RA Holvea M.C., Bell K.S., Hyman L.J., Avrova A.O., Whisson S.C.,  
RA Birch P.R.J., Toth I.K.;  
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL: BX950851; CAG75014.1;  
DR EMBL: BX950851; CAG75014.1;  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

RESULT 6

Q6RK52 PRELIMINARY; PRT; 479 AA.

ID Q6RK52  
AC Q6RK52;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HRPW.

GN Name=hrpW;  
OS Pectobacterium atrosepticum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=SCRI1039;  
RA Holvea M.C., Bell K.S., Hyman L.J., Avrova A.O., Whisson S.C.,  
RA Birch P.R.J., Toth I.K.;  
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL: AV496066; AAS20352.1;  
DR InterPro: IPR011050; Pectin lyase like.  
DR InterPro: IPR004898; Pect lyase.  
DR Pfam: PF03211; Pectate lyase; 1.  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

Query Match 43.5%; Score 1005; DB 2; Length 479;

Best Local Similarity 49.9%; Pred. No. 1.1e-43;  
Matches 231; Conservative 60; Mismatches 102; Indels 70; Gaps 15;

Qy 8 NNTSSPGLFQSGDNGLGHNSALGQDPIDRQTIQMAQLLAELLSL----- 59  
Db 61 NTPSSTDG--SSQQAQI-GNGSSALGQN-----GSAADMLKLEALIPSKNGQEA 110  
Qy 60 -SPQSGNAATGAGN---DQTTGVNAGLNGRKGTTAGTTTQSDSQNMLSEMNGNLDQA 115  
Db 111 GNPLSSGSSGAAGNSGASPLTSGSGAGVGGAQ-----NPEDLSRLQDSAGSALNNA 165  
Qy 116 ITPDQGGGGIGDNPPLKMLKLIARMQDSQDFQPGTGNNSSASGTSSSGSGSPFNDL 175  
Db 166 INPTADGGGQLSGNDLLKALLELIGNLMDSQKGEFGQP-----QSGSQSGGSGP--- 215  
Qy 176 SGKAPSGNSPNSVSTFSPSTPTSPSLDFPSSPTKAAG-----STPVTDPD 230  
Db 216 STG-APQASSGGGGSPAA-----PSAPSSVGGNGGAAPLTAAPT 257  
Qy 231 PV--GSAG-----IGAGNSVAFTSAGANQTVLHDTITVKAGQVFDGKGTFTAGSELGD 282  
Db 258 GVDGSAASPTASTAGAG-PVSPPTASANTVVDITIKVGFGEVFDGKGTFTAGSELGD 316  
Qy 283 GGQSENOKPLFIEDGASLKNVTMGDDGADGIHLGYDAKIDNLHVTNVGEDALTIVKPSA 342  
Db 317 GGQAGOKPLFELAQATLKNVFGDNDAGVHVRGDAKIDNVHVTNVGEDALTIVKPSN- 375  
Qy 343 GKSHVEITNSSEFHASDKILQNLADTNLSVDNVKADFGFTVTRNGGQGGNDLNLSHI 402  
Db 376 GKPAVEITNSAQAQSKIFQLNADANLTIDNFKAKDFGFTVTRNGGQGGNDLNLNSI 435  
Qy 403 SAEDGKFSVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKV 445  
Db 436 DAENGKFSVKSDSEGLNVKGNINLTNNVNNHYKVPDSANLQV 478

RESULT 7

Q6D5C8 PRELIMINARY; PRT; 479 AA.

ID Q6D5C8  
AC Q6D5C8;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Type III effector protein.  
GN Name=hrpW; ORFNames=ECA2112;





Db 362 CTNGKQFNDMSIELNGIDASHGKALVKSDSEDLKATGDIAMTDVKHAY 412

## RESULT 11

O87327 PRELIMINARY; PRT; 441 AA.  
AC O87327;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hrp type III secreted protein.  
GN Name=hrpW;  
OS Pseudomonas syringae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=317;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B728a;  
RX MEDLINE=98422476; PubMed=9748456;  
RA Charkowski A.O., Alfano J.R., Preston G., Yuan J., He S.Y.,  
RA Collmer A.;  
RT "The Pseudomonas syringae pv. tomato HrpW protein has domains similar  
RT to harpins and pectate lyases and can elicit the plant hypersensitive  
RT response and bind to pectate.";  
RL J. Bacteriol. 180:5211-5217(1998).  
DR EMBL; AF037983; AAC62530.1; -.  
DR HSSP; Q9RHW0; IE66.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0030570; F:pectate lyase activity; IEA.  
DR InterPro; IPR011050; Pectin lyas\_like.  
DR InterPro; IPR004898; Pect lyase.  
DR Pfam; PF03211; Pectate lyase; 1.  
DR SEQUENCE 441 AA; 44714 MW; 7B3B3146E51897BB CRC64;

Query Match 24.6%; Score 567.5; DB 2; Length 441;  
Best Local Similarity 36.4%; Pred. No. 2.4e-21;  
Matches 156; Conservative 46; Mismatches 133; Indels 93; Gaps 14;  
QY 36 QQPIDRQTI-----EQMAQLLAELLKSLLS---PQSGNAATGAGNDQTTGVGNAGLNGR 88  
DB 67 QNTDSSAATDPOSNVVKKLSALVTSLLQMLMNLKKQDTGQDSNEWQDPFQNEGGLG-- 124  
QY 89 KGTAGTTPQSDSQNMLSEMGNNGLDQAITPDGQGGQIGDNPLLKAMLKLIARMDGQSD 148  
DB 125 -----TPSA-----EGSDGGT-----QEA 138  
QY 149 QFGQPTGNNASGTSSTSGGSPFNDLSGKAPSGNSPS-----GNVSPVST-----FSPPS 200  
DB 139 SGDEGGGTTAATGDDGGGTSPTTEGDDG---GTSPTAEGDGGGYSVSTGADGSGAFS 194  
QY 201 TPTSPTSPLDPPSPPTKAGGSPVTDHPDP--VGSAGIGAGNSVAFTSAGANQ-----TV 254  
DB 195 T-----EDGTGGGGSGGVTPQVTPQANPGRNNGTGVSDTTGSLQSSEVVN 243  
QY 255 LHDITITVKAQVFDGKQGTFTAGSELGDDGQSQSENKQPLFILEDGASLKNVTMGDDGADGI 314  
DB 244 VKDTIKVGAQVFDGHGATFTADKSMGTGQDEHQKPLFELAGVALKNVNLGENEADGI 303  
QY 315 HLYGDAK-----IDNLHVTNVEDAITVKPNAGKSHVEITNSFEHASDKILOINAD 368  
DB 304 HV--NAKNSQVITDINVHAQNVGEMITVKGEGAKVTNLTNITNSANGADDKVIQLNAD 361  
QY 369 TNLSDNVNKAQDFTFVRTNGGQ--GNWDLNLGSHISAEDCKFSFKVSDSEGLNVNTSDIS 427  
DB 362 TLHKVDGFKATDFTGLVTRTNGGQFQDDMSVELNGVDATHGKFALVKSDSDDLKATGDI 421  
QY 428 LGDVENHY 435  
DB 422 MTDVKHAY 429

## RESULT 12

O87264 PRELIMINARY; PRT; 424 AA.  
AC O87264;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE HrpW.  
GN Name=hrpW;  
OS Pseudomonas syringae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=317;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DC3000;  
RX MEDLINE=98422476; PubMed=9748456;  
RA Charkowski A.O., Alfano J.R., Preston G., Yuan J., He S.Y.,  
RA Collmer A.;  
RT "The Pseudomonas syringae pv. tomato HrpW protein has domains similar  
RT to harpins and pectate lyases and can elicit the plant hypersensitive  
RT response and bind to pectate.";  
RL J. Bacteriol. 180:5211-5217(1998).  
DR EMBL; AF005221; AAC62526.1; -.  
DR HSSP; Q9RHW0; IE66.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0030570; F:pectate lyase activity; IEA.  
DR InterPro; IPR011050; Pectin lyas\_like.  
DR InterPro; IPR004898; Pect lyase.  
DR Pfam; PF03211; Pectate lyase; 1.  
DR SEQUENCE 424 AA; 42910 MW; 7AF4ED059BE79D2E CRC64;  
Query Match 24.2%; Score 559; DB 2; Length 424;  
Best Local Similarity 36.1%; Pred. No. 6.1e-21;  
Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps 13;  
QY 37 QPIDRQTIQMAQLLAELLKSL---LSPQSGNAATGAGNDQTTGVGNAGLNGRKGATG 93  
DB 72 KPNDSSQ--NTAKLISALIMSLQLMNLTKNSKKQDTNQCPDSQAFQNNGLG----- 122  
QY 94 TTPQSDSQNMLSEMGNNGLDQAITPDGQGGQIGDNPLLKAMLKLIARMDGQSDQFQGP 153  
DB 123 -TPSADS-----GGGG-----TPDATGGGG-GDTP-----SATGGG 151  
QY 154 GTGNNASGTSSTSGGSPFNDLSGKAPSGNSPSNYSPVSTFSPSTPTSTPLDPPS 213  
DB 152 GGDITPTATGGGGGGGGTPTATGGG---SGGTPTATGGGEGGVTPQITPOL-----A 200  
QY 214 SPTKAAGGSTPTVDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDITITVKAQGVFDGKGT 273  
DB 201 NPNRTSG-----TGVSVDTAGS-----TEQAGKINVVKDTIKVGAQVFDGHGAT 245  
QY 274 FTAGSELGDDGQSQSENKQPLFILEDGASLKNVTMGDDGADGIHLYG-----DAKIDNLHVTN 329  
DB 246 FTADKSMGNGDQGENKQKPMFELAEATLKNVNLGENEVDGIHVKAQNAQEVITDINVHAQN 305  
QY 330 VGEDAITVKPNAGKSHVEITNSFEHASDKILOINADTNLSVDNVKAKDFTFVRTNG 389  
DB 306 VGEDLITVKGEGGAATVNLNKNSSAKGADDKVVQVQLNANTHLKIDNFKADDFGTWVRTNG 365  
QY 390 GQO--GNWDLNLGSHISAEDCKFSFKVSDSEGLNVNTSDISLGDVENHY 435  
DB 366 GKQFDDMSIELNGIEANHGKFALVKSDSDDLKATGNIAWTVDVKHAY 412

## RESULT 13

O7C4I5 PRELIMINARY; PRT; 424 AA.  
AC O7C4I5; Q7BM42;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Type III helper protein HrpW (Pto) (HrpW).



```

Db 146 GUTP-----TATGN-----TPSVEGSSND--DGVTPQLANP 176
QY 187 SGNYSPVSTFSPPTSPSTPLDPSPSKAAGGTPVTDHPDPVGSAGIGAGNSVAPT 246
Db 177 N-----HTSGTGPVSD-----187
QY 247 SAGANQ-----TVLHDTITVKAQVDPKGQFTTAGSELGCGQSGENQKPLFILEDGASL 301
Db 188 TAGANDQAGKVIWVKDTIKVAANTVYDAHGATFTADKSMGNGDQSGENQKPLPELAGATL 247
QY 302 KNVVTMGDDGADGIHLYG-DAK---IDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSPEH 357
Db 248 KNAVLENEVDGIHVAKAKDAQVQITDINVAENVGEDMITVKGEGAKVTNLQIKNSSAEN 307
QY 358 ASDKILQNLNADTNLSVDNVKADFGFTVRTNGQQ--GNWDLNLSHISAEDGKFSFVKSDS 416
Db 308 ADDKVFQNLNANVHLNITGEANNFTGLVKTNGEKQFDDMNKLDGVDANHGKFAVVKSDS 367
QY 417 EGLNVNTSDISLGDVENHY 435
Db 368 E-----DLQLGDQQRH 379

RESULT 15
Q8KKZ2
ID Q8KKZ2 PRELIMINARY; PRT; 307 AA.
AC Q8KKZ2;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein hrpW.
GN Name=hrpW;
OS Rhizobium etli.
OC Plasmid symbiotic plasmid p42d.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CFN42;
RX MEDLINE=91193195; PubMed=2013564;
RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;
RT "Structural complexity of the symbiotic plasmid of Rhizobium
leguminosarum bv. phaseoli.";
RL J. Bacteriol. 173:2411-2419(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CFN42;
RX MEDLINE=97419521; PubMed=9274036;
RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
RA Cevallos M.A., Davila G.;
RT "Sequence, localization and characteristics of the replicator region
of the symbiotic plasmid of Rhizobium etli.";
RL Microbiology 143:2825-2831(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=CFN42;
RX MEDLINE=22309397; PubMed=12421308;
RA Quintero V., Cevallos M.A., Davila G.;
RT "A site-specific recombinase (RinQ) is required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etli.";
RL Mol. Microbiol. 46:1023-1032(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=CFN42;
RX Ramirez M.A., Bustos P., Girard L., Rodriguez O., Cevallos M.A.,
RA Davila G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=CFN42;
RX Quintero V., Bustos P., Davila G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

```

```

RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RA Gonzalez V., Bustos P., Medrano-Soto A., Ramirez-Romero M.A.,
RA Romero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Cellis J.C.,
RA Quintero V., Girard L.L., Rodriguez O., Flores M., Cevallos M.A.,
RA Collado-Vides J., Davila G.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RA Quintero V., Bustos P., Davila G.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80928; AAM54988.1; -.
DR HSP; Q9RH00; IE86.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0030570; E:pectate lyase activity; IEA.
DR InterPro; IPR011050; Pectin_lyas_like.
DR InterPro; IPR004898; Pectate_lyase.
DR Pfam; PF03211; Pectate_lyase; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 307 AA; 32912 MW; ED8844FA3A3A5E98 CRC64;

Query Match 18.3%; Score 423.5; DB 2; Length 307;
Best Local Similarity 37.7%; Fred. No. 3.6e-14;
Matches 121; Conservative 48; Mismatches 83; Indels 69; Gaps 14;

QY 144 DQSQDFQPGQGTGNNSASGTS---SSGSGSPNDLSGGKAPSGNSPNSPVSTFSPS 200
Db 22 DLESCLG-----GSNRADTFTITRKVSPPEDF-----SGNPPT-----LTSVVPNS 66
QY 201 TPTS-----PTGPLDF-----PSSPTKAAGGSTPVTDHPDPVGSAGIGAGN 241
Db 67 RETSENGMDSDPKDLLRKHINWQSDSKVDPSEKQATTLQT-TTEKPD-----114
QY 242 SVAFTSAGANQTVLHDTITVKAQVDFCKGQFTTAGSELGCGQSGENQKPLFILEDGASL 301
Db 115 ----LSKSGSVIWNNEPIVDDGG-VFDGKGATYTTASSKLGGGQSETQSPFLIKNGATL 169
QY 302 KNVVTMGDDGADGIHLYGDAKIDNLHVTNVGDEDAITVKPNSAGKSHVEITNSSFHASDK 361
Db 170 KNVVDLGENGADGIHYVDGATLENVWQNVGEDALTVK--SAG---DITIIGSAGKATDK 224
QY 362 ILQLNADTNLSVDNVKADFGFTVRTNGQQGNWDLNLSHISAEDGKFS-----FVKSDSE 417
Db 225 IPQINADTRFYLKDFVADGFTLVRTNGKQIDAD-----VTIDGGAFSHGSNVRFTDSS 279
QY 418 GLNVN-TSDISLGDVENHYKV 437
Db 280 LASVTFLSDITLDDVKNWTRV 300

```

Search completed: January 25, 2005, 16:09:21

Job time : 200 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 19:24:24 ; Search time 47.5096 Seconds  
(without alignments)  
203.868 Million cell updates/sec

Title: DESAI-879\_31\_57

Perfect score: 128

Sequence: 1 NSALGQPIDRDTIQMAQLLAELIKS 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003Bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	447	2	Aaw96260 Hypersens
2	128	100.0	447	3	Aay71094 Erwinia a
3	128	100.0	447	3	Aay84855 A hyperse
4	128	100.0	447	5	Aao22548 Hypersens
5	128	100.0	447	5	Aae18296 Erwinia a
6	128	100.0	447	5	Aae16448 E. amylov
7	128	100.0	447	5	Abb9226 Erwinia a
8	52	40.6	313	7	ABO73754 Pseudomon
9	52	40.6	457	7	ABO73936 Pseudomon
10	52	40.6	710	8	ADN73161 Thale cre
11	51	39.8	660	7	ADP29258 Bacterial
12	51	39.8	660	7	Adg32467 Pasteurel
13	51	39.8	1312	2	Aaw22775 Human RAD
14	51	39.8	1312	2	Aaw71295 Human hom
15	51	39.8	1318	5	Abb77985 Amino aci
16	51	39.8	1318	7	Adj68860 Human hea
17	51	39.8	1318	8	ADJ66509 RAD50 hom
18	50.5	39.5	266	5	ABG70071 Human pre
19	50.5	39.5	352	2	AAW22307 Lipase mo
20	50.5	39.5	596	5	ABG61825 Prostate
21	50.5	39.5	596	7	ADB75398 Prostate
22	50	39.1	430	5	ABB47515 Listeria
23	49	38.3	264	7	ABO71596 Pseudomon
24	49	38.3	697	6	ABR40712 Oryza sat
25	49	38.3	3249	6	ABU39648 Protein e

26	48.5	37.9	237	7	ABO70264	Abo70264 Pseudomon
27	48.5	37.9	777	7	ADC03511	Adc03511 Pseudomon
28	48.5	37.9	891	7	ABO76849	Abo76849 Pseudomon
29	48	37.5	223	4	ABB60921	Abb60921 Drosophil
30	48	37.5	320	8	ADH13660	Adh13660 Human ENZ
31	48	37.5	422	6	ABP59216	Abp59216 Human dru
32	48	37.5	492	5	ABG69596	Abg69596 Human NOV
33	48	37.5	492	7	ADJ83019	Adj83019 Human NOV
34	48	37.5	495	7	ADJ83077	Adj83077 Human cyt
35	48	37.5	630	6	ABU21525	Abu21525 Protein e
36	48	37.5	1419	5	Aao20572	Aao20572 Protein E
37	48	37.5	1419	6	ABR99408	AbR99408 Amino aci
38	48	37.5	1419	8	ADN48494	Adn48494 Human smg
39	48	37.5	1449	7	ADJ70004	Adj70004 Human hea
40	48	37.5	2246	6	ABU41616	Abu41616 Protein e
41	47	36.7	112	7	ABO63216	Abo63216 Klebsiell
42	47	36.7	183	8	ADN47050	Adn47050 Thermococ
43	47	36.7	301	8	ADN97661	Adn97661 S ambofac
44	47	36.7	320	1	ADP80242	Adp80242 Sequence
45	47	36.7	320	1	AAP80714	Aap80714 Sequence

#### ALIGNMENTS

RESULT 1  
AAW96260  
ID AAW96260 standard; protein; 447 AA.  
XX  
AC AAW96260;  
XX  
DT 14-JUN-1999 (first entry)  
XX  
DE Hypersensitive response eliciting protein (HrpW).  
XX  
KW Hypersensitive response elicitor protein; hypersensitive response; hrpW;  
KW pathogen; infection; crop protection; disease resistance;  
KW pest resistance; transgenic plant; colouration; maturation.  
XX  
OS Erwinia amylovora.  
XX  
PN WO9907208-Al.  
XX  
PD 18-FEB-1999.  
XX  
PF 27-JUL-1998; 98WO-US015547.  
XX  
PR 06-AUG-1997; 97US-0055108P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Kim JF, Beer SV;  
XX  
DR WPI: 1999-167126/14.  
DR N-PSDB; AAX09007.  
XX  
PT New Erwinia amylovora hypersensitive response eliciting gene and protein  
PT - useful for providing transgenic plants and seeds with enhanced growth,  
PT and insect and disease resistance.  
XX  
PS Claim 1; Page 50-51; 54pp; English.  
XX  
CC The hypersensitive response eliciting protein (hrp) or polypeptide is  
CC produced as part of an active defense by plants against incompatible  
CC pathogen infections. The hypersensitive response is a rapid localised  
CC necrosis. The hrp protein and gene when used in nucleotide constructs are  
CC useful for providing disease resistance to plants, insect control to  
CC plants, and enhancing plant growth (enhancing fruit size and earlier  
CC colouration and maturation), by direct application of the protein to  
CC plants, or by producing transgenic plants or seeds using the hrp gene  
XX  
SQ Sequence 447 AA;

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#### THE CONCEPT OF THE "CITY"

PP 06-NOV-2001; 2001WO-US043715.  
 XX  
 PR 13-NOV-2000; 2000US-0248169P.  
 XX  
 PA (EDEN-) EDEN BIOSCIENCE CORP.  
 XX  
 PI Wei Z, Leon E, Oviedo A;  
 XX  
 DR WPI; 2002-575194/61.  
 DR N-PSDB; AAL41133.  
 XX  
 PT Inhibiting desiccation of cuttings from ornamental plants, by treating  
 PT ornamental plants with hypersensitive response elicitor protein, or  
 PT expressing heterologous hypersensitive response elicitor protein in  
 PT plants.  
 XX  
 PS Disclosure; Page 12-13; 69pp; English.  
 XX  
 CC The invention relates to a method for inhibiting desiccation of cuttings  
 CC from ornamental plants. The method involves treating the cuttings with a  
 CC hypersensitive response elicitor protein or polypeptide, or providing a  
 CC transgenic ornamental plant or plant seed transformed with a DNA molecule  
 CC encoding the hypersensitive response elicitor polypeptide, and growing  
 CC the ornamental plant or transgenic ornamental plant produced from the  
 CC transgenic ornamental plant seed. The hypersensitive response elicitor  
 CC protein or polypeptide is useful for inhibiting desiccation of cuttings  
 CC from ornamental plants, for harvesting cuttings from ornamental plants,  
 CC for promoting early flowering of ornamental plants, and enhancing the  
 CC longevity of flower blooms on ornamental plant cuttings. This sequence  
 CC represents a hypersensitive response elicitor protein of the invention  
 XX  
 SQ Sequence 447 AA;  
 Query Match 100.0%; Score 128; DB 5; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-11;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NSALGQOPIDRQTIEQMAQLLAELLS 27  
 DB 31 NSALGQOPIDRQTIEQMAQLLAELLS 57  
 RESULT 5  
 AAEL18296  
 ID AAEL18296 standard; protein; 447 AA.  
 XX  
 AC AAEL18296;  
 XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Erwinia amylovora hypersensitive response elicitor (HRE) #2.  
 XX  
 KW Hypersensitive response elicitor; HRE; transgenic plant; plant growth;  
 KW stress tolerance; disease tolerance; modified flower colour;  
 KW insect resistance; herbicide resistance; male sterility.  
 XX  
 OS Erwinia amylovora.  
 XX  
 PN WO200195724-A2.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 13-JUN-2001; 2001WO-US018955.  
 XX  
 PR 15-JUN-2000; 2000US-0211585P.  
 XX  
 PA (EDEN-) EDEN BIOSCIENCE CORP.  
 XX  
 PI Wei Z, Derocher J;  
 XX  
 DR WPI; 2002-130707/17.  
 DR N-PSDB; AAD29125.  
 XX

PT Improving effectiveness of transgenic plants by topical application of a  
 PT hypersensitive response elicitor protein to the transgenic plant or by  
 PT incorporating into the plant a transgene encoding the protein.  
 XX  
 PS Disclosure; Page 13-14; 86pp; English.  
 XX  
 CC The invention relates to methods of improving the effectiveness of  
 CC transgenic plants which involves either topical application of a  
 CC hypersensitive response elicitor (HRE) protein to the transgenic plant or  
 CC incorporating into the transgenic plant a transgene encoding HRE. HRE  
 CC sequence is used for improving the effectiveness of transgenic plants by  
 CC maximising the benefit of transgenic traits associated with a deleterious  
 CC effect on growth, stress tolerance, disease or insect resistance.  
 CC enhanced growth, herbicide resistance, male sterility, modified flower  
 CC colour and biochemically modified plant product in the transgenic plants  
 CC or overcoming the deleterious effects. The present sequence is Erwinia  
 CC amylovora HRE protein  
 XX  
 SQ Sequence 447 AA;  
 Query Match 100.0%; Score 128; DB 5; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-11;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NSALGQOPIDRQTIEQMAQLLAELLS 27  
 DB 31 NSALGQOPIDRQTIEQMAQLLAELLS 57  
 RESULT 6  
 AAEL16448  
 ID AAEL16448 standard; protein; 447 AA.  
 XX  
 AC AAEL16448;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE E. amylovora hypersensitive response elicitor protein #2.  
 XX  
 KW Hypersensitive response elicitor protein; plant growth; fruit coloration;  
 KW disease resistance; stress resistance; phytotoxin; insect infection;  
 KW plant maturation.  
 XX  
 OS Erwinia amylovora.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 5..64  
 FT /label= Hypersensitive\_response\_eliciting\_domain\_1  
 FT Region 5..45  
 FT /label= Acidic\_unit  
 FT Region 45..64  
 FT /label= Alpha\_helix  
 FT Domain 103..146  
 FT /label= Hypersensitive\_response\_eliciting\_domain\_2  
 FT Region 103..131  
 FT /label= Acidic\_unit  
 FT Region 131..146  
 FT /label= Alpha\_helix  
 XX  
 PN WO200198501-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 12-JUN-2001; 2001WO-US018820.  
 XX  
 PR 16-JUN-2000; 2000US-0212211P.  
 XX  
 PA (EDEN-) EDEN BIOSCIENCE CORP.  
 XX  
 PI Fan H, Wei Z;  
 XX  
 DR WPI; 2002-122282/16.  
 DR N-PSDB; AAD27016.  
 XX

XX New hypersensitive response elicitor proteins comprising spaced apart  
PT domains having an acidic portion linked to an alpha-helix, useful for  
PT imparting disease or stress resistance, controlling insects or enhancing  
PT plant growth.  
XX  
PS Disclosure; Page 13-14; 99pp; English.  
XX  
XX The patent discloses hypersensitive response elicitor proteins and  
CC nucleotides encoding such proteins. Hypersensitive response elicitor  
CC proteins comprise an isolated pair or more of spaced apart domains, each  
CC comprising an acidic portion linked to an alpha-helix and capable of  
CC eliciting a hypersensitive response in plants. Sequences of the invention  
CC are used to impart disease resistance to plants, to enhance plant growth,  
CC to control insects and/or to impart stress resistance to plants which  
CC includes resistance to environmental stresses such as climate, air  
CC pollution, chemical and nutritional stress. The method of imparting  
CC disease resistance has the potential for treating previously untreatable  
CC diseases, treating diseases systemically and avoiding the use of  
CC infectious agents or environmentally harmful materials. Hyper- sensitive  
CC response elicitor sequences are used to enhance plant growth which  
CC encompasses greater yield, increased in quantity of seeds produced,  
CC percentage of seeds germinated, plant size and biomass, bigger fruits,  
CC earlier fruit coloration and plant maturation. They are also used for  
CC insect control which encompasses preventing direct insect damage to plant  
CC by feeding injury, interfering with insect larval feeding on the plants,  
CC preventing insects from colonising host plants and releasing phytotoxins.  
CC Sequences of the invention also prevent subsequent disease damage to  
CC plants resulting from insect infection. The present sequence is Erwinia  
CC amylovora hypersensitive response elicitor protein  
XX  
XX Sequence 447 AA;

Query Match 100.0%; Score 128; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 6.4e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NSALGQQPIDRQTIEQMAQLLAELLS 27  
DB 31 NSALGQQPIDRQTIEQMAQLLAELLS 57

RESULT 7  
ABB09226  
ID ABB09226 standard; protein; 447 AA.  
XX ABB09226;  
XX  
XX 08-JUL-2002 (first entry)  
XX  
XX Erwinia amylovora hypersensitive response elicitor SEQ ID NO:5.  
XX  
XX Hypersensitive response elicitor; fruit; vegetable; plant; desiccation;  
KW postharvest disease.  
XX  
XX Erwinia amylovora.  
XX  
XX WO200180639-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 17-APR-2001; 2001WO-US012468.  
XX  
XX 19-APR-2000; 2000US-0198359P.  
XX  
XX (EDEN-) EDEN BIOSCIENCE CORP.  
XX  
XX Wei Z, Qiu D, Remick D;  
XX  
XX WPI; 2002-041357/05.  
DR N-PSDB; ABL51711.  
XX  
XX Inhibiting post harvest disease (caused by Penicillium, Botrytis,  
PT

PT Phytophthora, or Erwinia) or desiccation and enhancing the longevity in a  
PT fruits or vegetables, using hypersensitive response elicitor proteins or  
PT nucleic acids.  
XX  
XX Disclosure; Page 11-12; 72pp; English.  
XX  
XX The present invention describes methods for inhibiting post harvest  
CC disease or desiccation and enhancing the longevity in a fruits or  
CC vegetables, using hypersensitive response elicitor proteins or  
CC polypeptides or nucleic acids (I) derived from pathogens (e.g. Erwinia  
CC amylovora, E. stewartii, E. chrysanthemi, E. carotovora, Xanthomonas,  
CC Pseudomonas syringae, P. solanacearum, Phytophthora, and Clavibacter).  
CC (I) has bactericidal activity, and can be used in gene therapy. The  
CC method can be used for inhibiting post harvest disease (caused by  
CC Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and  
CC enhancing the longevity in a fruits or vegetables. The method enables  
CC growers, warehouse packers, shippers and suppliers to process, handle and  
CC store fruit and vegetables with reduced losses caused by post harvest  
CC disease and desiccation, therefore reducing costs to the consumer and  
CC improving quality. The present sequence represents a hypersensitive  
CC response elicitor protein given in the exemplification of the present  
CC invention

XX Sequence 447 AA;

Query Match 100.0%; Score 128; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 6.4e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSALGQQPIDRQTIEQMAQLLAELLS 27  
DB 31 NSALGQQPIDRQTIEQMAQLLAELLS 57

RESULT 8

ABB073754  
ID ABB073754 standard; protein; 313 AA.

XX ABB073754;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #5929.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

KW Pseudomonas aeruginosa.

OS US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR N-PSDB; ABD07325.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 22500; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC





```
CC invention.
XX
SQ Sequence 710 AA;
    Query Match          40.6%; Score 52; DB 8; Length 710;
    Best Local Similarity 44.4%; Pred. No. 50;
    Matches 12; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 NSALGOQPIDROTIEQMAQLLAELKLS 27
    ||||| ||||| ::|||::|||:
Db 56 NSAFSQESDRAAKRAKATQVLAEAKN 84

RESULT 11
ADF29258
ID ADF29258 standard; protein; 660 AA.
XX
AC ADF29258;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial virulence associated Pasteurella multocida protein PM1459.
XX
KW antibacterial; vaccine; mutant; Gram negative bacterium; mutation;
KW attenuated virulence; immunogenic composition; passive immunization;
KW insertion site; transposon tagged mutagenesis.
XX
OS Pasteurella multocida.
XX
PI EP1350796-A1.
XX
PD 08-OCT-2003.
XX
PF 05-APR-2002; 2002EP-00290861.
XX
PR 05-APR-2002; 2002EP-00290861.
XX
PA (MERI-) MERIAL.
XX
PI Crooke HR, Shea JE, Feldman RG, Goutebroze SG, Le Gros F;
XX
DR WPI; 2003-781146/74.
XX
DR N-PSDB; ADF29257.
XX
PT New attenuated mutant of a Gram-negative bacteria, useful for the
PT production of immunogenic or vaccine compositions for the prevention of
PT bacterial infections, particularly Gram negative bacteria.
XX
PS Example 4; SEQ ID NO 50; 96pp; English.
XX
CC The invention relates to a mutant Gram negative bacterium (Pasteurella
CC multocida) comprising a mutation in a nucleotide sequence which codes for
CC a polypeptide having an identity which is equal or more than 70%, 75%,
CC 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% with an amino acid sequence
CC encoded by any of 29 fully defined sequences of 267-2832 bp, given in the
CC specification, the mutation resulting in attenuated virulence of the
CC bacterium. The attenuated mutant is useful for the production of
CC immunogenic or vaccine compositions for the prevention of bacterial
CC infections, particularly Gram negative bacteria. The antibody preparation
CC is useful for the production of a passive immunization composition of a
CC therapeutic composition against Gram-negative bacteria. This sequence
CC represents the Pasteurella multocida protein PM0773 which is involved in
CC bacterial virulence.
XX
SQ Sequence 660 AA;
    Query Match          39.8%; Score 51; DB 7; Length 660;
    Best Local Similarity 55.0%; Pred. No. 65;
    Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 QPIDROTIEQMAQLLAELL 25
    ||||| ::|||::|||:
Db 178 QQPHNKQIEQLKKLQOELL 197

RESULT 12
ADG32467
ID ADG32467 standard; protein; 660 AA.
XX
AC ADG32467;
XX
DT 26-FEB-2004 (first entry)
XX
DE Pasteurella multocida PM1459 protein, a homologue of PM70 SeqID 50.
XX
KW immunogenic; vaccine; bacterial infection; Pasteurellaceae; immunogen;
KW allergen; growth factor; cytokine; antibacterial;
KW transposon insertion site; attenuated gram negative bacteria.
XX
OS Pasteurella multocida.
XX
PI WO2003086277-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010308.
XX
PR 05-APR-2002; 2002US-0370282P.
XX
PR 03-APR-2003; 2003US-00406686.
XX
PA (MERI-) MERIAL LLC.
XX
PI Crooke HR, Shea JE, Feldman RG, Goutebroze SG, Legros F;
XX
DR WPI; 2003-845250/78.
XX
DR N-PSDB; ADG32466.
XX
PT New mutant gram negative bacterium having attenuated virulence, useful
PT for preparing a composition or vaccine for preventing bacterial
PT infections.
XX
PS Example 4; SEQ ID NO 50; 170pp; English.
XX
CC This invention relates to novel live attenuated gram negative bacteria
CC useful for immunogenic compositions and in vaccines to prevent bacterial
CC infections. Specifically, it refers to a mutant gram negative bacterium
CC from the Pasteurellaceae family, having a mutation in a first nucleotide
CC sequence that codes for a first polypeptide, and results in the bacterium
CC having attenuated virulence. This mutation can be a deletion, insertion
CC or replacement of nucleic acids in a regulatory element or coding
CC sequence of a gene that encodes an immunogen such as a viral, parasitic
CC or bacterial agent, allergen, growth factor, therapeutic protein or
CC cytokine. The present invention describes a method for attenuating live
CC bacteria that reduces or abolishes pathogenicity, decreases bacterial
CC growth rate and thereby prevents cell death. Accordingly, these
CC compositions have antibacterial activity and can be administered in an
CC antibody preparation. This polypeptide sequence is a homologue of the
CC Pasteurella multocida PM70 protein that is disrupted by insertion of a
CC transposon to generate a mutant of the invention.
XX
SQ Sequence 660 AA;
    Query Match          39.8%; Score 51; DB 7; Length 660;
    Best Local Similarity 55.0%; Pred. No. 65;
    Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 QPIDROTIEQMAQLLAELL 25
    ||||| ::|||::|||:
Db 178 QQPHNKQIEQLKKLQOELL 197

RESULT 13
AAW22775
ID AAW22775 standard; protein; 1312 AA.
XX
AC AAW22775;
```

XX 21-DEC-1998 (first entry)  
 XX DE Human RAD50.  
 XX KW Human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;  
 XX KW central nervous system.  
 XX OS Homo sapiens.  
 XX PN WO9727284-A2.  
 XX PD 31-JUL-1997.  
 XX PF 24-JAN-1997; 97WO-US001299.  
 XX PR 26-JAN-1996; 96US-00592126.  
 XX PR 17-JUL-1996; 96US-00687080.  
 XX PA (GENE-) GENELABS TECHNOLOGIES INC.  
 XX PI Dolganov G;  
 XX DR WPI; 1997-393672/36.  
 XX DR N-PSDB; AAT75237.  
 XX PT Human tumour suppressor gene RAD50 - useful to detect predisposition to,  
 XX PT decrease risk of and treat cancer, also Septin-2 homologues.  
 XX PS Claim 5; Page 82-86; 195pp; English.  
 XX CC The human RAD50 (hRAD50) is involved in DNA repair and has tumour  
 CC suppression activity, can be used to detect predisposition to, decrease  
 CC the risk of or treat cancers, e.g. acute myeloid leukaemia,  
 CC myelodysplastic syndrome, therapy related myelodysplastic syndrome,  
 CC therapy related acute myeloid leukaemia, refractory anaemia or refractory  
 CC anaemia with excess blasts. Also disclosed in this invention is Human  
 CC Septin-2 homologues of which may be used as targets for cancer therapies  
 CC and central nervous system directed treatment methods, and to measure the  
 CC proliferative potential of selected cell types  
 XX SQ Sequence 1312 AA;  
 Query Match 39.8%; Score 51; DB 2; Length 1312;  
 Best Local Similarity 47.4%; Pred. No. 1.4e+02;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 9 IDROTIEQMAQLLAELKLS 27  
 Db 1237 LDRENIESLAHALVEIKS 1255  
 RESULT 14  
 AAW71295  
 ID AAW71295 standard; protein; 1312 AA.  
 XX AC AAW71295;  
 XX DT 25-NOV-1998 (first entry)  
 XX DE Human homologue of yeast RAD50.  
 XX KW Human homologue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetase;  
 KW immunomodulatory activity; identification; activated T-cell.  
 XX OS Homo sapiens.  
 XX PN WO9838306-A1.  
 XX PD 03-SEP-1998.  
 XX PF 27-FEB-1997; 97WO-US003159.  
 XX

PR 27-FEB-1997; 97WO-US003159.  
 XX (GENE-) GENELABS TECHNOLOGIES INC.  
 XX PI Dolganov G;  
 XX DR WPI; 1998-481207/41.  
 XX DR N-PSDB; AAV59979.  
 XX PT Novel human immunomodulatory poly:peptide(s) - have homology to the yeast  
 XX PT RAD50 or Drosophila Septin-2 proteins.  
 XX PS Disclosure; Page 136-140; 155pp; English.  
 XX CC The present sequence represents a human homologue of the yeast S.  
 CC cerevisiae gene RAD50. The present sequence has 35% overall homology to  
 CC the yeast RAD50 gene, and is expressed in activated T-cells, testis,  
 CC foetal liver and heart tissues. The specification also describes  
 CC sequences encoding human homologues of the yeast RAD50, the Drosophila  
 CC Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory  
 CC activity. The nucleic acids and proteins can be used to identify  
 CC activated T-cells in a sample population. They can also be used to  
 CC isolate and identify sequences encoding other proteins or other compounds  
 CC having immunomodulatory activity  
 XX SQ Sequence 1312 AA;  
 Query Match 39.8%; Score 51; DB 2; Length 1312;  
 Best Local Similarity 47.4%; Pred. No. 1.4e+02;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 9 IDROTIEQMAQLLAELKLS 27  
 Db 1237 LDRENIESLAHALVEIKS 1255  
 RESULT 15  
 ABB77985  
 ID ABB77985 standard; protein; 1318 AA.  
 XX AC ABB77985;  
 XX DT 22-OCT-2002 (first entry)  
 XX DE Amino acid sequence of a human RAD50 homologue.  
 XX KW Nucleic acid integration; homologous recombination; telomeric region;  
 KW RAD50.  
 XX OS Homo sapiens.  
 XX PN EP1217074-A1.  
 XX PD 26-JUN-2002.  
 XX PF 22-DEC-2000; 2000EP-00204693.  
 XX PR 22-DEC-2000; 2000EP-00204693.  
 XX PA (UYLE-) RIJKSUNIV LEIDEN.  
 XX PA (BINA-) STICHTING BINAIR VECTOR SYSTEEM.  
 XX PI Hooykaas PJJ, Van Attikum H, Bundock P;  
 XX WPI; 2002-550409/59.  
 XX PT Directing integration of nucleic acid of interest to a sub-telomeric  
 PT region in an eukaryote with preference for non-homologous recombination,  
 PT by steering an integration pathway towards homologous recombination.  
 XX PS Disclosure; Fig 5; 63pp; English.  
 XX CC The specification describes a method for directing integration of a

CC nucleic acid of interest to a pre-determined site, where the nucleic acid  
CC has homology at or around the pre-determined site, in a eukaryote with a  
CC preference for non-homologous recombination. The method comprises  
CC steering an integration pathway towards homologous recombination. The  
CC method is useful for directing integration of a nucleic acid of interest  
CC to a subtelomeric and/or telomeric region in an eukaryote with a  
CC preference for non-homologous recombination. The nucleic acid of interest  
CC comprises an inactive gene to replace an active gene, or vice versa, is a  
CC portion of a gene delivery vehicle, confers a desired property to the  
CC eukaryotic cell, or encodes a therapeutic proteinaceous substance or a  
CC substance conferring resistance for an antibiotic substance to a cell.  
CC The method is useful for improving gene targeting efficiency. The method  
CC is useful in the replacement of an active gene by an inactive gene, for  
CC e.g. for the inactivation of genes controlling undesired side branches of  
CC metabolic pathways, to increase the quality of bulk products such as  
CC starch, or to increase the production of specific secondary metabolites  
CC or to inhibit formation of unwanted metabolites, and also to inactive  
CC genes controlling senescence in fruits and flowers or that determine  
CC flower pigments. The method is also useful for replacing an inactive gene  
CC by an active gene. For e.g. the replacement of a defective p53 by an  
CC intact p53. Many tumours acquire a mutation in p53 during their  
CC development which renders it inactive and often correlates with a poor  
CC response to cancer therapy. By replacing the defect p53 by an intact p53,  
CC e.g. through gene therapy, conventional anti cancer therapy have better  
CC changes of succeeding. The method is also useful for therapeutic  
CC proteinaceous substance integration. A tumoricidal gene can be delivered  
CC to a pre-determined site present only in e.g. proliferating cells, or  
CC present only in tumour cells, e.g. to the site where a tumour antigen is  
CC expressed form. ABB77984-86 represent RAD50 homologues. RAD50 is involved  
CC in non-homologous recombination  
XX

SQ Sequence 1318 AA;

Query Match 39.8%; Score 51; DB 5; Length 1318;  
Best Local Similarity 47.4%; Pred. NO. 1.4e+02;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 IDRTTTEOMALLAELLKS 27  
          |||:|||||:|:|:|:  
Db 1243 LDRENTESLAHALVEIKS 1261

Search completed: January 25, 2005, 20:30:25  
Job time : 54.5096 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 20:14:24 ; Search time 19.7308 Seconds  
(without alignments)  
90.751 Million call updates/sec

Title: DESAI-879\_31\_57

Perfect score: 128

Sequence: 1 NSALGQPIDROTIEQMALLAEILKS 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B COMB.pap.\*

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4: /cgn2\_6/prodata/1/iaa/6B COMB.pap.\*

5: /cgn2\_6/prodata/1/iaa/PCUS COMB.pap.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	447	3	US-09-120-927-2
2	128	100.0	447	4	US-09-431-614-6
3	52	40.6	313	4	US-09-252-991A-22500
4	52	40.6	457	4	US-09-252-991A-22682
5	51	39.8	1312	2	US-08-592-126-148
6	51	39.8	1312	2	US-08-687-080-51
7	51	39.8	1312	4	US-09-168-595-148
8	49	38.3	173	4	US-09-270-767-40996
9	49	38.3	173	4	US-09-270-767-56212
10	49	38.3	264	4	US-09-252-991A-20342
11	48.5	37.9	237	4	US-09-252-991A-19010
12	48.5	37.9	891	4	US-09-252-991A-25595
13	47	36.7	112	4	US-09-489-039A-9733
14	47	36.7	620	4	US-09-252-991A-23615
15	45	35.2	605	3	US-08-982-785A-10
16	45	35.2	620	4	US-09-629-498-10
17	45	35.2	631	4	US-09-252-991A-20418
18	45	35.2	686	3	US-08-982-785A-8
19	45	35.2	686	4	US-09-629-498-8
20	45	35.2	756	3	US-08-982-785A-2
21	45	35.2	756	4	US-09-629-498-2
22	45	35.2	1084	3	US-09-227-725A-3
23	45	35.2	1225	4	US-09-501-171-4
24	45	35.2	1247	4	US-09-501-171-6
25	44.5	34.8	122	4	US-09-248-796A-28164
26	44	34.4	120	4	US-09-107-532A-4295
27	44	34.4	255	4	US-09-252-991A-31162

28	44	34.4	319	1	US-08-125-746-1	Sequence 1, Appli
29	44	34.4	319	4	US-08-948-276-2	Sequence 2, Appli
30	44	34.4	320	1	US-08-125-746-3	Sequence 3, Appli
31	44	34.4	320	4	US-08-948-276-1	Sequence 1, Appli
32	44	34.4	320	6	5225537-4	Patent No. 5225537
33	44	34.4	325	4	US-09-248-796A-20030	Sequence 20030, A
34	44	34.4	325	4	US-09-324-096A-2	Sequence 2, Appli
35	44	34.4	327	3	US-09-324-096A-6	Sequence 4, Appli
36	44	34.4	327	3	US-09-324-096A-6	Sequence 6, Appli
37	44	34.4	328	4	US-09-248-796A-24205	Sequence 24205, A
38	44	34.4	378	4	US-09-710-279-1428	Sequence 1428, Ap
39	44	34.4	378	3	US-09-134-001C-3248	Sequence 3248, Ap
40	44	34.4	457	4	US-08-924-629C-6	Sequence 6, Appli
41	44	34.4	502	4	US-10-101-464A-945	Sequence 945, App
42	44	34.4	635	4	US-09-252-991A-20298	Sequence 20298, A
43	43	33.6	93	4	US-09-489-039A-7880	Sequence 7880, Ap
44	43	33.6	190	4	US-09-252-991A-29854	Sequence 29854, A
45	43	33.6	315	4	US-09-252-991A-31381	Sequence 31381, A

ALIGNMENTS

RESULT 1

US-09-120-927-2

; Sequence 2, Application US/09120927

; Patent No. 6262018

; GENERAL INFORMATION:

; APPLICANT: Kim, Jihyun Francis

; APPLICANT: Beer, Steven V

; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Nixon, Haigraive, Devans & Doyle LLP

; STREET: P.O. Box 1051, Clinton Square

; CITY: Rochester

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 14603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/120,927

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/055,108

; FILING DATE: 06-AUG-1977

; ATTORNEY/AGENT INFORMATION:

; NAME: Goldman, Michael L.

; REGISTRATION NUMBER: 30,727

; REFERENCE/DOCKET NUMBER: 19603/1581

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (716) 263-1304

; TELEFAX: (716) 263-1600

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 447 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-120-927-2

Query Match 100.0%; Score 128; DB 3; Length 447;

Best Local Similarity 100.0%; Pred. No. 6.5e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSALGQPIDROTIEQMALLAEILKS 27

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Db 31 NSALGQPIDRTIEQMAQLLAELLS 57
|||||
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22682
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22682

Query Match 40.6%; Score 52; DB 4; Length 457;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 4 LGQOPIDRTIEQMAQLLAEL 25
|||:|:|:|:|:|
Db 312 LGQSPLLAALAEELLQLLAEML 333
|||:|:|:|:|:|

RESULT 5
US-08-592-126-148
; Sequence 148, Application US/08592126
; Patent No. 5821091
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54
US-08-592-126-148

Query Match 39.8%; Score 51; DB 2; Length 1312;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 9 IDRTIEQMAQLLAELLS 27
|||:|:|:|:|:|

Db 31 NSALGQPIDRTIEQMAQLLAELLS 57
|||||
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22500
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22500

Query Match 40.6%; Score 52; DB 4; Length 313;
Best Local Similarity 55.6%; Pred. No. 3.3;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QPIDRTIEQMAQLLAEL 24
|||:|:|:|:|:|
Db 21 QRLERQVVAQVLAEL 38
|||:|:|:|:|:|

RESULT 4
US-09-252-991A-22682
; Sequence 22682, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22500
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22500

Query Match 40.6%; Score 52; DB 4; Length 313;
Best Local Similarity 55.6%; Pred. No. 3.3;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QPIDRTIEQMAQLLAEL 24
|||:|:|:|:|:|
Db 21 QRLERQVVAQVLAEL 38
|||:|:~|:~|:~|:~|

RESULT 4
US-09-252-991A-22682
; Sequence 22682, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```



[illegible]



```

RESULT 15
US-08-982-785A-10
; Sequence 10, Application US/08982785A
; Patent No. 6258929
; GENERAL INFORMATION:
; APPLICANT: Kosik, Kenneth S.
; APPLICANT: Zhou, Jianhua
; TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
; TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,785A
; FILING DATE: 02-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,556
; FILING DATE: 02-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29, 066
; REFERENCE/DOCKET NUMBER: 05311/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-982-785A-10

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
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Title: DESAI-879\_31\_57

Perfect score: 128

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	128	100.0	447	9	US-09-835-684-5
2	128	100.0	447	9	US-09-880-371-5
3	128	100.0	447	9	US-09-879-248-6
4	128	100.0	447	14	US-10-010-390-5
5	128	100.0	447	15	US-10-441-736-6
6	128	100.0	447	17	US-10-847-142-5
7	51	39.8	660	15	US-10-406-686A-50
8	51	39.8	1312	14	US-10-393-602-148
9	51	39.8	1318	16	US-10-408-765A-666
10	50.5	39.5	266	14	US-10-043-487-245
11	50.5	39.5	596	14	US-10-205-823-222
12	49	38.3	628	16	US-10-437-963-174471
13	49	38.3	697	14	US-10-183-687-244

14	49	38.3	3249	15	US-10-282-122A-67572	Sequence 67572, A
15	48.5	37.9	211	17	US-10-425-115-328898	Sequence 328898,
16	48	37.5	96	17	US-10-425-115-267186	Sequence 267186,
17	48	37.5	470	14	US-10-369-493-4813	Sequence 4813, Ap
18	48	37.5	478	14	US-10-369-493-7572	Sequence 7572, Ap
19	48	37.5	492	14	US-10-032-189-10	Sequence 10, Appl
20	48	37.5	495	14	US-10-032-189-68	Sequence 68, Appl
21	48	37.5	630	15	US-10-282-122A-49449	Sequence 49449, A
22	48	37.5	1419	16	US-10-473-115-2	Sequence 2, Appl
23	48	37.5	1449	16	US-10-408-765A-1810	Sequence 1810, Ap
24	48	37.5	2246	15	US-10-282-122A-69540	Sequence 69540, A
25	47	36.7	83	15	US-10-424-539-147641	Sequence 147641,
26	46	35.9	31	16	US-10-745-069-52	Sequence 52, Appl
27	46	35.9	31	17	US-10-768-288A-52	Sequence 52, Appl
28	46	35.9	31	17	US-10-780-325A-52	Sequence 52, Appl
29	46	35.9	32	16	US-10-869-649-52	Sequence 51, Appl
30	46	35.9	32	16	US-10-745-069-51	Sequence 51, Appl
31	46	35.9	32	17	US-10-768-288A-51	Sequence 51, Appl
32	46	35.9	32	17	US-10-780-325A-51	Sequence 51, Appl
33	46	35.9	32	17	US-10-869-649-51	Sequence 51, Appl
34	46	35.9	33	16	US-10-745-069-50	Sequence 50, Appl
35	46	35.9	33	17	US-10-768-288A-50	Sequence 50, Appl
36	46	35.9	33	17	US-10-780-325A-50	Sequence 50, Appl
37	46	35.9	33	17	US-10-869-649-50	Sequence 50, Appl
38	46	35.9	34	16	US-10-745-069-49	Sequence 49, Appl
39	46	35.9	34	17	US-10-768-288A-49	Sequence 49, Appl
40	46	35.9	34	17	US-10-780-325A-49	Sequence 49, Appl
41	46	35.9	34	17	US-10-869-649-49	Sequence 49, Appl
42	46	35.9	36	16	US-10-745-069-47	Sequence 47, Appl
43	46	35.9	36	17	US-10-768-288A-47	Sequence 47, Appl
44	46	35.9	36	17	US-10-780-325A-47	Sequence 47, Appl
45	46	35.9	36	17	US-10-869-649-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-09-835-684-5  
; Sequence 5, Application US/09835684  
; Patent No. US20020019337A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Qiu, Dewen  
; TITLE OF INVENTION: REMICK, Dean  
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE  
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR  
; TITLE OF INVENTION: DESICCATION  
; FILE REFERENCE: 21829/71  
; CURRENT APPLICATION NUMBER: US/09/835,684  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/198,359  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
US-09-835-684-5

Query Match 100.0%; Score 128; DB 9; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSALGQPIDRTIETQMAQLLAELLS 27

DB 31 NSALGQPIDRTIETQMAQLLAELLS 57

RESULT 2

US-09-880-371-5  
; Sequence 5, Application US/09880371

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; Patent No. US20020059658A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: DeRoche, Jay
; TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 21829/91
; CURRENT APPLICATION NUMBER: US/09/880,371
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,585
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-09-880-371-5

Query Match      100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 NSALGQQPIDRQTIEQMAQLLAELLKS 27
Db 31 NSALGQQPIDRQTIEQMAQLLAELLKS 57

RESULT 3
US-09-879-248-6
; Sequence 6, Application US/09879248
; Patent No. US20020062500A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Hao
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21829/81
; CURRENT APPLICATION NUMBER: US/09/879,248
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/212,211
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-09-879-248-6

Query Match      100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

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Db 31 NSALGQQPIDRQTIEQMAQLLAELLKS 57

RESULT 4
US-10-010-390-5
; Sequence 5, Application US/10010390
; Publication No. US20030104979A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Leon, Ernesto
; APPLICANT: Oviedo, Agustín
; TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
; TITLE OF INVENTION: FROM ORNAMENTAL PLANTS
; FILE REFERENCE: 21829/111
; CURRENT APPLICATION NUMBER: US/10/010,390
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/248,169
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-010-390-5

Query Match      100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 NSALGQQPIDRQTIEQMAQLLAELLKS 27
Db 31 NSALGQQPIDRQTIEQMAQLLAELLKS 57

RESULT 5
US-10-441-736-6
; Sequence 6, Application US/10441736
; Publication No. US20040016029A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Schading, Richard L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/203 (RBC-003)
; CURRENT APPLICATION NUMBER: US/10/441,736
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/107,243
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/431,614
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-441-736-6

Query Match      100.0%; Score 128; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

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Db 31 NSALGQQPIDRQTIEQMAQLLAELLKS 57

RESULT 6
US-10-847-142-5
; Sequence 5, Application US/10847142
; Publication No. US20040265442A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Qiu, Dewen
; APPLICANT: Remick, Dean
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
; TITLE OF INVENTION: DESICCATION
; FILE REFERENCE: 21829/197
; CURRENT APPLICATION NUMBER: US/10/847,142
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/198,359
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/835,684
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-847-142-5

Query Match      100.0%; Score 128; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 NSALGQQPIDRQTIEQMAQLLAELLKS 27
Db 31 NSALGQQPIDRQTIEQMAQLLAELLKS 57
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; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-847-142-5

Query Match      100.0%; Score 128; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSALGQPIDRQTIEQMAQLLAELLS 27
Db 31 NSALGQPIDRQTIEQMAQLLAELLS 57

RESULT 7
US-10-406-686A-50
; Sequence 50, Application US/10406686A
; Publication No. US20040033586A1
; GENERAL INFORMATION:
; APPLICANT: CROOKE, HELEN RACHEL
; APPLICANT: SHEA, JACQUELINE ELIZABETH
; APPLICANT: FELDMAN, ROBERT GRAHAM
; APPLICANT: COUTEBROZE, SYLVAIN GABRIEL
; APPLICANT: LEGRAS, FRANCOIS-XAVIER
; TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA
; FILE REFERENCE: 454313-3171.1
; CURRENT APPLICATION NUMBER: US/10/406,686A
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/370,282
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-406-686A-50

Query Match      39.8%; Score 51; DB 15; Length 660;
Best Local Similarity 55.0%; Pred. No. 83;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 QQPIDRQTIEQMAQLLAELL 25
Db 178 QQPHNKQIEQLKQLQOELL 197

RESULT 8
US-10-393-602-148
; Sequence 148, Application US/10393602
; Publication No. US20030170714A1
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory Polypeptides
; NUMBER OF SEQUENCES: 151.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/393,602
; FILING DATE: 19-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
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; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Rad50, pro-translation of SEQ ID NO:54
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-10-393-602-148

Query Match      39.8%; Score 51; DB 14; Length 1312;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 IDRTIEQMAQLLAELLS 27
Db 1237 LDRENIESLAHALVEIILS 1255

RESULT 9
US-10-408-765A-666
; Sequence 666, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 1318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-666

Query Match      39.8%; Score 51; DB 16; Length 1318;
Best Local Similarity 47.4%; Pred. No. 1.9e+02;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 IDRTIEQMAQLLAELLS 27
Db 1243 LDRENIESLAHALVEIILS 1261

RESULT 10
US-10-043-487-245
; Sequence 245, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypepti
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
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Wed Jan 26 08:08:27 2005

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; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174471
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72408C.1.pap
; US-10-437-963-174471

Query Match 38.3%; Score 49; DB 16; Length 628;
Best Local Similarity 43.3%; Pred. No. 1.6e+02; Indels 4; Gaps 1;
Matches 13; Conservative 4; Mismatches 9;

Qy 1 NSALGQPIDROT----IEQMAQLLAELK 26
Db 415 NDAMDQPPSDCLTRVRLLEQYASTIAELVK 444

RESULT 13
US-10-183-687-244
; Sequence 244, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Farnoud, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BB1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 244
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-183-687-244

Query Match 38.3%; Score 49; DB 14; Length 697;
Best Local Similarity 43.3%; Pred. No. 1.8e+02; Indels 4; Gaps 1;
Matches 13; Conservative 4; Mismatches 9;

Qy 1 NSALGQPIDROT----IEQMAQLLAELK 26
Db 484 NDAMDQPPSDCLTRVRLLEQYASTIAELVK 513

; Publication No. US/10/043,487
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Shigella Flexneri
; US-10-043-487-245

Query Match 39.5%; Score 50.5; DB 14; Length 266;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 12; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 NSALGQ-QPIDROTIEQMAQ 19
Db 60 NSALGQTPSDQDTLVQRAE 79

RESULT 11
US-10-205-823-222
; Sequence 222, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 222
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-205-823-222

Query Match 39.5%; Score 50.5; DB 14; Length 596;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 12; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 NSALGQ-QPIDROTIEQMAQ 19
Db 390 NSALGQTPSDQDTLVQRAE 409

RESULT 12
US-10-437-963-174471
; Sequence 174471, Application US/10437963
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RESULT 14
US-10-282-122A-67572
; Sequence 67572, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67572
; LENGTH: 3249
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (650)..(650)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1081)..(1081)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1088)..(1088)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1114)..(1114)
; OTHER INFORMATION: X=any amino acid
; US-10-282-122A-67572

Query Match 38.1%; Score 49; DB 15; Length 3249;
Best Local Similarity 61.1%; Pred. No. 1e+03;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 10 DRQTIEQMAQLLAELLS 27
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Db 2637 DRQTIEQMARHWRNLQA 2654
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RESULT 15
US-10-425-115-328898
; Sequence 328898, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 328898
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(211)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_63023C.1.pep
; US-10-425-115-328898

Query Match 37.9%; Score 48.5; DB 17; Length 211;
Best Local Similarity 39.4%; Pred. No. 52;
Matches 13; Conservative 4; Mismatches 3; Indels 13; Gaps 1;

QY 3 ALGOQPIDQTIEQ-----MAQLLA 22
|||||:|:|
Db 156 ALGOQPIDRVGLEKEAATLSRMGLRTLAQVLA 188

Search completed: January 25, 2005, 20:58:03
Job time : 66.1635 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 20:02:44 ; Search time 15.3173 Seconds  
(without alignments)  
169.602 Million cell updates/sec

Title: DESAI-879\_31\_57

Perfect score: 128

Sequence: 1 NSALGQPIDRTIEQMAQLLAELLS 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	447	T18447	HrpW protein - Erw
2	51	39.8	580	G69656	2-succinyl-6-hydro
3	51	39.8	1312	T30845	probable DNA repai
4	50	39.1	430	AE1803	sugar binding prot
5	50	39.1	430	AF1429	sugar binding prot
6	50	39.1	2706	T28155	variant-specific s
7	49	38.3	257	S76537	hypothetical prote
8	49	38.3	902	AH2999	conserved hypothet
9	49	38.3	903	A96284	hypothetical prote
10	48.5	37.9	213	C82953	hypothetical prote
11	48.5	37.9	627	S76462	hypothetical prote
12	48.5	37.9	762	H83348	probable acylase p
13	48	37.5	350	S76212	hypothetical prote
14	47	36.7	246	D87487	uridylylate kinase l
15	47	36.7	356	S01992	glutenin low molec
16	47	36.7	817	T01866	hypothetical prote
17	47	36.7	1122	T28130	hypothetical prote
18	46	35.9	36	PCBO	pancreatic hormone
19	46	35.9	59	1 FCSH	pancreatic hormone
20	46	35.9	75	G91013	hypothetical prote
21	46	35.9	75	A85858	hypothetical prote
22	46	35.9	75	B64988	hypothetical 8.3 k
23	46	35.9	159	A82720	conserved hypothet
24	46	35.9	159	A97502	hypothetical prote
25	46	35.9	409	S76119	hypothetical prote
26	46	35.9	792	T29187	hypothetical prote
27	45.5	35.5	249	A81001	electron transfer
28	45.5	35.5	249	F82018	electron transfer
29	45.5	35.5	929	S75098	hypothetical prote

30	45	35.2	36	1	A61132	pancreatic hormone
31	45	35.2	36	1	C61132	pancreatic hormone
32	45	35.2	36	1	D61132	pancreatic hormone
33	45	35.2	66	1	PCCT	Mut7/mudix family
34	45	35.2	203	2	C95194	mutator protein (i
35	45	35.2	203	2	H98060	conserved hypothet
36	45	35.2	455	2	B72339	hypothetical prote
37	45	35.2	510	2	AG2985	sugar ABC transpor
38	45	35.2	511	2	H98297	hypothetical prote
39	45	35.2	595	2	G96491	conserved hypothet
40	45	35.2	605	2	A82381	polysubonucleotide
41	45	35.2	705	2	S70691	conserved hypothet
42	45	35.2	978	2	B89971	neural plakophilin
43	45	35.2	1247	2	T42209	hypothetical prote
44	45	35.2	1818	1	S73852	hypothetical prote
45	44.5	34.8	397	2	T52302	COP9 signalosome c

ALIGNMENTS

RESULT 1

T18447

HrpW protein - Erwinia amylovora

C:Species: Erwinia amylovora

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T18447

R:Gaudriault, S.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z18936

A:Accession: T18447

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-447 <CAU>

A:Cross-references: UNIPROT:O54508; EMBL:Y13831; NID:el293450; PID:el293451; PIDN:CAA74

A:Experimental source: strain CFP1430; specific host Pommoideae

C:Genetics:

A>Note: hrpW

Query Match

Best Local Similarity 100.0%; Score 128; DB 2; Length 447;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSALGQPIDRTIEQMAQLLAELLS 27

DB 31 NSALGQPIDRTIEQMAQLLAELLS 57

RESULT 2

G69656

2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (EC 4.1.1.3.-) [validated]

N:Alternate names: menCF protein; menD protein

N:Contains: 2-oxoglutarate decarboxylase (EC 4.1.1.71)

C:Species: Bacillus subtilis

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004

C:Accession: G69656; S27509; S27510; T46640; T46641

R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hulio, M.F

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segnioni, J.; Sekowska, A.; Sero

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, J.; Tosato, V.; Uchiyama

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: G69656

<b>A;Residues:</b> 1-1312 <KIM>					
<b>A;Cross-references:</b> UNIPROT:P70388; EMBL:U66887; NID:g1575574; PID:g1575575; PIDN:AAC528					
<b>C;Genetics:</b>					
<b>A;Gene:</b> RAD50					
<b>A;Map position:</b> 11					
<b>C;Superfamily:</b> RAD50 protein					
<b>C;Keywords:</b> DNA repair					
<b>Query Match</b>		39.8%;	Score 51;	DB 2;	Length 1312;
<b>Best Local Similarity</b>		47.4%;	Pred.No. 55;		
<b>Matches</b>		9;	Conservative	5;	Mismatches 0; Gaps 0;
<b>Qy</b>	9 IDRTIQEQMAQLLAELLS 27 :::     :    ::   Db     1237 LDRENIESLAHVEILKS 1255				
<b>RESULT 4</b>					
<b>AE1803</b>					
sugar binding protein (ABC transporter) homolog lin2972 [imported] - Listeria innocua (t					
<b>C;Species:</b> Listeria innocua					
<b>C;Date:</b> 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004					
<b>C;Accession:</b> AE1803					
<b>R;Glaser,</b> P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,					
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.					
D.; Jones, L.M.; Karst, U.					
<b>Science</b> 294, 849-852, 2001					
<b>A;Authors:</b> Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Me					
Ok, C.; Schluerter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,					
<b>A;Title:</b> Comparative genomics of Listeria species.					
<b>A;Reference number:</b> AB1077; PMID:21537279; PMID:11679669					
<b>A;Accession:</b> AE1803					
<b>A;Status:</b> preliminary					
<b>A:Molecule type:</b> DNA					
<b>A;Residues:</b> 1-430 <GLA>					
<b>A;Cross-references:</b> UNIPROT:O926R9; GB:AL592022; PIDN:CAC98197.1; PID:g16415512; GSPDB:(					
<b>A;Experimental source:</b> strain Clip11262					
<b>C;Genetics:</b>					
<b>A;Gene:</b> lin2972					
<b>Query Match</b>		39.1%;	Score 50;	DB 2;	Length 430;
<b>Best Local Similarity</b>		39.1%;	Pred.No. 23;		
<b>Matches</b>		9;	Conservative	7;	Mismatches 0; Indels 0; Gaps 0;
<b>Qy</b>	5 GQQPIDRTIQEQMAQLLAELLS 27     ::: ::    ::   Db     341 GAQPYNKEVVEQAKYNEVIKS 363				
<b>RESULT 5</b>					
<b>AF1429</b>					
sugar binding protein (ABC transporter) homolog lmc2839 [imported] - Listeria monocytoc					
<b>C;Species:</b> Listeria monocytogenes					
<b>C;Date:</b> 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004					
<b>C;Accession:</b> AF1429					
<b>R;Glaser,</b> P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,					
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.					
D.; Jones, L.M.; Karst, U.					
<b>Science</b> 294, 849-852, 2001					
<b>A;Authors:</b> Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma					
Ok, C.; Schluerter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,					
<b>A;Title:</b> Comparative genomics of Listeria species.					
<b>A;Reference number:</b> AB1077; PMID:21537279; PMID:11679669					
<b>A;Accession:</b> AF1429					
<b>A;Status:</b> preliminary					
<b>A:Molecule type:</b> DNA					
<b>A;Residues:</b> 1-430 <GLA>					
<b>A;Cross-references:</b> UNIPROT:QBY3J6; GB:NC_003210; PIDN:CAD01052.1; PID:g16412339; GSPDB					
<b>A;Experimental source:</b> strain EGD-e					
<b>C;Genetics:</b>					
<b>A;Gene:</b> lmc2839					
<b>Query Match</b>		39.1%;	Score 50;	DB 2;	Length 430;

Best Local Similarity 39.1%; Pred. No. 23;  
Matches 9; Conservative 7; Mismatches 0; Gaps 0;

QY 5 GQOPIRQRTIEQMAQLLAELLS 27  
| | | | | : | | | | | : | | | | |  
Db 341 GAQPVNKVEVQKAYKENEVIKS 363

RESULT 6  
T28155  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragmented)  
A:Alternate names: erythrocyte membrane binding protein 1 (EMP1)  
C:Species: Plasmodium falciparum  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28155  
R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.  
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement  
A:Reference number: Z20477; MUID:97373957; PMID:9230440  
A:Accession: T28155  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2706 <ROW>  
A:CROSS-references: UNIPROT:O15870; EMBL:Y13402; PIDN:CAA73831.1  
A:Experimental source: strain IT 4/25/5  
C:Genetics:  
A:Introns: 2493/3  
A>Note: R29R+var1

Query Match 39.1%; Score 50; DB 2; Length 2706;  
Best Local Similarity 47.6%; Pred. No. 1.6e+02;  
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 5 GQOPIRQRTIEQMAQLLAELL 25  
| | | | | : | | | | | : | | | | |  
Db 2108 GKTFFDAQNFQMGQTAKEFV 2128

RESULT 7  
S76537  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
A:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76537  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76537  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-257 <KAN>  
A:CROSS-references: UNIPROT:Q55741; EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA1038  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 38.3%; Score 49; DB 2; Length 257;  
Best Local Similarity 54.5%; Pred. No. 18;  
Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 LGOQPIRQRTIEQMAQLLAELL 25  
| | | | | : | | | | | : | | | | |  
Db 177 LGOQQQKRRSIQWAFLLGNLL 198

RESULT 8  
AH2999  
conserved hypothetical protein Atu3602 [imported] - Agrobacterium tumefaciens (strain C58)  
C:Species: Agrobacterium tumefaciens  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AH2999

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.;  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan,  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AH2999  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-902 <KUR>  
A:CROSS-references: UNIPROT:Q8U9X3; GB:AE008689; PIDN:AAL44414.1; PID:g17742013; GSPDB:  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3602  
A:Map position: linear chromosome

Query Match 38.3%; Score 49; DB 2; Length 902;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GQOPIRQRTIEQMAQLLAEL 24  
| | | | | : | | | | | : | | | | |  
Db 723 GQOQSDQMTAEQRLDALKNL 742

RESULT 9  
A96284  
hypothetical protein AGR\_L\_2452 [imported] - Agrobacterium tumefaciens (strain C58, Cer  
C:Species: Agrobacterium tumefaciens  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: A96284  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: A96284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-903 <KUR>  
A:CROSS-references: UNIPROT:Q8U9X3; GB:AE007870; PIDN:AAK89795.1; PID:g15159723; GSPDB:  
C:Genetics:  
A:Gene: AGR\_L\_2452  
A:Map position: linear chromosome

Query Match 38.3%; Score 49; DB 2; Length 903;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GQOPIRQRTIEQMAQLLAEL 24  
| | | | | : | | | | | : | | | | |  
Db 724 GQOQSDQMTAEQRLDALKNL 743

RESULT 10  
CB2953  
hypothetical protein PA5534 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: CB2953  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lln,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: CB2953  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-213 <STO>  
A:CROSS-references: UNIPROT:Q9HT40; GB:AE004966; GB:AE004091; NID:g9951872; PIDN:AAG0891

Wed Jan 26 08:08:27 2005

```
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5534

Query Match      37.9%; Score 48.5; DB 2; Length 213;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY  2  SALGOQ-PIDRTIOMQAQLLAELLK 26
Db   2  SALPOEKPLPRQAFDDFQVLAELVR 27

RESULT 11
S76462
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76462
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-627 <KAN>
A:Cross-references: UNIPROT:P74489; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAAI859
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      37.9%; Score 48.5; DB 2; Length 627;
Best Local Similarity 37.0%; Pred. No. 56;
Matches 10; Conservative 8; Mismatches 6; Indels 3; Gaps 1;

QY  2  SALGOQPIDRQTI---EQMAQLLAELL 25
Db   322  TTLGQPFVIBATVVKQSQQLIVEVL 348

RESULT 12
H83348
probable acylase PA2385 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83348
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bu
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83348
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-762 <STO>
A:Cross-references: UNIPROT:Q91194; GB:AE004664; GB:AE004091; NID:g9948415; PIDN:AAG0577
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA2385

Query Match      37.9%; Score 48.5; DB 2; Length 762;
Best Local Similarity 32.3%; Pred. No. 69;
Matches 10; Conservative 9; Mismatches 3; Indels 9; Gaps 1;

QY  5  GQOPIDRTIOMQA-----QLLAELLK 26
Db   523  GKQPLEAKTLEMTANHVSADQVLPDLR 553

RESULT 13
```

```
S76212
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76212
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KAN>
A:Cross-references: UNIPROT:P74376; EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAAI84;
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      37.5%; Score 48; DB 2; Length 350;
Best Local Similarity 40.7%; Pred. No. 36;
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY  1  NSALGQOPIDRTIOMQAQLLAELLKS 27
Db   133  NSSIGQIQIERQSTSATPOASPEILPS 159

RESULT 14
D87487
uridylylate kinase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87487
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Iaub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: UNIPROT:Q9A705; GB:AE005673; NID:g13423374; PIDN:AAK23896.1; GSPDB:
C:Genetics:
A:Gene: CC1921
C:Superfamily: uridylylate kinase

Query Match      36.7%; Score 47; DB 2; Length 246;
Best Local Similarity 38.5%; Pred. No. 34;
Matches 10; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY  4  LGOQP--IDRTIOMQAQLLAELLKS 27
Db   23  MGDTPYGIDNTVQSVAEVAVIVKS 48

RESULT 15
S01992
glutenin low molecular weight chain precursor - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01992
R:Pitts, E.G.; Rafalski, J.A.; Hedgcoth, C.
Nucleic Acids Res. 16, 11376, 1988
A:Title: Nucleotide sequence and encoded amino acid sequence of a genomic gene region f
A:Reference number: S01992; MUID:89083577; PMID:3205747
A:Accession: S01992
A:Molecule type: DNA
A:Residues: 1-356 <PIT>
A:Cross-references: UNIPROT:P10385; EMBL:X07747; NID:g21782; PIDN:CAA30570.1; PID:g2178
C:Superfamily: gliadin
```

Query Match 36.7%; Score 47; DB 2; Length 356;  
Best Local Similarity 58.8%; Pred. No. 50;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 4 LGGQPIDROTIEQMAQL 20  
| | | | : | | | |  
Db 301 LGGQPPQQQLAHQIAQL 317

Search completed: January 25, 2005, 20:36:58  
Job time : 16.3173 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 19:58:54 ; Search time 85.4135 Seconds  
(without alignments)  
181.881 Million cell updates/sec

Title: DESAI-879\_31\_57  
Perfect score: 128  
Sequence: 1 NSALGQQPIDRQTIEQMAQLLAELLS 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	138	2 Q79AW7	Q79AW7 erwinia amy
2	128	100.0	447	2 O54508	O54508 erwinia amy
3	128	100.0	447	2 Q9LAW2	Q9LAW2 erwinia amy
4	109	85.2	450	2 Q6XDB8	Q6XDB8 erwinia pyr
5	109	85.2	450	2 AAQ17046	AAQ17046 erwinia p
6	109	85.2	450	2 AAS45453	AAS45453 erwinia p
7	61.5	48.0	1214	2 Q8DZ21	Q8DZ21 synchococc
8	53	41.4	416	2 Q6DEJ7	Q6DEJ7 brachydanio
9	53	41.4	440	2 Q6IQ77	Q6IQ77 brachydanio
10	53	41.4	440	2 AAH71533	AAH71533 brachydan
11	53	41.4	943	2 Q7SBG5	Q7SBG5 neurospora
12	52.5	41.0	452	2 Q8U310	Q8U310 pyrococcus
13	51	39.8	377	2 Q7SY40	Q7SY40 brachydanio
14	51	39.8	413	2 Q7NH72	Q7NH72 gloeobacter
15	51	39.8	498	2 Q8JHT9	Q8JHT9 brachydanio
16	51	39.8	580	1 MEND BACSU	P23970 b menaquinio
17	51	39.8	660	2 Q9CKZ1	Q9CKZ1 pasteurella
18	51	39.8	845	2 Q8BT55	Q8BT55 mus musculus
19	51	39.8	911	2 Q8BTF7	Q8BTF7 mus musculus
20	51	39.8	1017	2 Q6VG40	Q6VG40 chimpanzee
21	51	39.8	1017	2 AAR02377	AAR02377 chimpanzee
22	51	39.8	1173	2 Q9UP86	Q9UP86 homo sapien
23	51	39.8	1312	2 Q92878	Q92878 homo sapien
24	51	39.8	1312	2 P70388	P70388 mus musculus
25	51	39.8	1312	2 Q9J1L8	Q9J1L8 rattus norv
26	51	39.8	1318	2 Q43254	Q43254 homo sapien
27	50.5	39.5	352	1 LIFO PSEWI	O05938 pseudomonas
28	50.5	39.5	596	1 ENH HUMAN	Q96hc4 homo sapien
29	50.5	39.5	596	2 AAT06739	AAT06739 homo sapi
30	50.5	39.5	1283	2 Q7UM20	Q7UM20 rhodopirell
31	50	39.1	430	2 Q926r9	Q926r9 listeria in

32 50 39.1 430 2 Q8Y3J6 listeria mo  
33 50 39.1 430 2 Q71VS2 listeria mo  
34 50 39.1 430 2 AAT05594 listeria  
35 50 39.1 544 2 Q97473 caenorhabdi  
36 50 39.1 559 2 Q882U6 pseudomonas  
37 50 39.1 2706 2 O15870 plasmodium  
38 49.5 38.7 477 2 Q6FJC5 candida gla  
39 49 38.3 257 2 Q55741 synchocyst  
40 49 38.3 305 2 Q88Y51 lactobacill  
41 49 38.3 358 2 Q824U8 chlamydophi  
42 49 38.3 457 2 Q7X5J7 leuconostoc  
43 49 38.3 560 2 Q804Z3 fugu rubrip  
44 49 38.3 628 2 Q84LF4 oryza sativ  
45 49 38.3 687 2 Q81MA8 drosophila

#### ALIGNMENTS

##### RESULT 1

Q79AW7 PRELIMINARY; PRT; 138 AA.  
AC Q79AW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW (Fragment).  
GN Name=hrpW;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Es321;  
RX MEDLINE=98115919; PubMed=9448330;  
RA Bogdanove A.J., Kim J.F., Wei Z., Kolchinsky P., Charkowski A.O.,  
RA Conlin A.K., Collmer A., Beer S.V.;  
RT "Homology and functional similarity of an hrp-linked pathogenicity  
RT locus, dspB, of Erwinia amylovora and the avirulence locus avrE of  
RT Pseudomonas syringae pathovar tomato.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:1325-1330(1998).  
DR EMBL; U97504; AAC04849.1; -.  
FT NON\_TER  
FT 138  
SQ SEQUENCE 138 AA; 13788 MW; 4FE17177C74B3C6 CRC64;

Query Match 100.0%; Score 128; DB 2; Length 138;  
Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

##### QY 1 NSALGQQPIDRQTIEQMAQLLAELLS 27

|||||  
31 NSALGQQPIDRQTIEQMAQLLAELLS 57

##### RESULT 2

O54508 PRELIMINARY; PRT; 447 AA.  
AC O54508;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW protein.  
GN Name=hrpW;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CFBP1430;  
RX MEDLINE=98086111; PubMed=9426142;  
RA Gaudriault S., Malandrin L., Paulin J.P., Barny M.A.;

```
DR InterPro; IPR011050; Pectin_lyas_like.  
DR InterPro; IPR004898; Pect_lyase.  
DR Pfam; PF03211; Pectate_lyase; 1  
SQ SEQUENCE 447 AA; 45540 MW; 0BBAEA3971EDC2F6 CRC64;
```

RA Hur J. H., Lim C. K.;  
RT "Molecular characterization hrp genes cluster of *Erwinia* put  
RT and expression of hrpGp encoding elicitor of the hypersens  
RT response.";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY237642; AAQ17046.1; -.



```

SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;
Query Match 85.2%; Score 109; DB 2; Length 450;
Best Local Similarity 88.5%; Pred. No. 1.6e-06;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSALGOQPIDROTIEQMAQLLAELLK 26
|||||
Db 31 NSAQGHPIDROTIEQMAQLLGELLK 56

RESULT 6
AAS45453 PRELIMINARY; PRT; 450 AA.
AC AAS45453;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE HRPW.
DE HRPW.
GN HRPW.
OS Erwinia pyrifoliae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Erwinia.
OX NCBI_TaxID=79967;
RN [1]_TaxID=79967;
RP SEQUENCE FROM N.A.
RC STRAIN=WT3;
RA Shrestha R., Baek S.J., Park D.H., Bae H.N., Cho J.M., Hwang I.,
RA Hur J.H., Lim C.K.;
RT "Identification of hrp genes cluster and characterization of HR
RT elicitor hrpNEP gene in Erwinia pyrifoliae.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY530755; AAS45453.1; -.
SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;

Query Match 85.2%; Score 109; DB 2; Length 450;
Best Local Similarity 88.5%; Pred. No. 1.6e-06;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSALGOQPIDROTIEQMAQLLAELLK 26
|||||
Db 31 NSAQGHPIDROTIEQMAQLLGELLK 56

RESULT 7
Q8DGZ1 PRELIMINARY; PRT; 1214 AA.
AC Q8DGZ1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hydatonase / oxoprolinase.
GN OrderedLocusNames=tlx2171;
OS Synchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=32046;
RN [1]_TaxID=32046;
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneo T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; AF005376; BAC09723.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002821; Hydatonase A.
DR InterPro; IPR003692; Hydatonase B.
DR InterPro; IPR008040; Hydatonase B.
DR Pfam; PF01968; Hydatonase_A; 1.

DR PFam; PF02538; Hydatonase_B; 1.
DR Pfam; PF05378; Hydatonase_A; 1.
KW Complete proteome.
SQ SEQUENCE 1214 AA; 129918 MW; 929531C290F24447 CRC64;

Query Match 48.0%; Score 61.5; DB 2; Length 1214;
Best Local Similarity 54.2%; Pred. No. 15;
Matches 13; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 5 GOQPIDROTIE-QMAQLLAELLK 27
|||||
Db 395 GOQPLDRDSVEQFAQLRQEIYRS 418

RESULT 8
Q6DEJ7 PRELIMINARY; PRT; 416 AA.
AC Q6DEJ7;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077115; AAH77115.1; -.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 47726 MW; 008C38F5B606CE42 CRC64;

Query Match 41.4%; Score 53; DB 2; Length 416;
Best Local Similarity 38.5%; Pred. No. 79;
Matches 10; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 NSALGOQPIDROTIEQMAQLLAELLK 26
|||||
Db 57 NFGGLKKSIESRVLESQYLIAMLK 82

RESULT 9
Q6IQ77 PRELIMINARY; PRT; 440 AA.
ID Q6IQ77
AC Q6IQ77;
```

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05-JUL-2004 (TREMBLrel. 27, Created)
05-JUL-2004 (TREMBLrel. 27, Last sequence update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
Zgc:86915.
Name=zgc:86915;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Boasak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Faney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Embryo;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
-I- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; BC071533; AAH71533.1; -.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP450I.
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PRINTS; PRG0385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 440 AA; 50312 MW; DID4740B1IEFF183 CRC64;
Query Match 41.4%; Score 53; DB 2; Length 440;
Best Local Similarity 42.3%; Pred. No. 84;
Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
OY 1 NSALGQQPIDRQTTEOMQAQLLELLK 26
|:::|:::|:::|
Db 81 NFGLGKGKSIESRVLESQYLFAELLK 106
RESULT 10
AAH71533 PRELIMINARY; PRT; 440 AA.
ID AAH71533
AC AAH71533;
DT 01-JUN-2004 (TREMBLrel. 27, Created)
DT 01-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]

```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 19:24:24 ; Search time 43.9904 Seconds  
(without alignments)  
203.868 Million cell updates/sec

Title: DESAI-879\_116\_140  
Perfect score: 128  
Sequence: 1 ITPDGGGQIGDNPFLKAMKLIA 25

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	447	AAW96260	Hypersens
2	128	100.0	447	AAW71094	Erwinia a
3	128	100.0	447	AAW84855	A hyperse
4	128	100.0	447	AAO22548	Hypersens
5	128	100.0	447	AAE18296	Erwinia a
6	128	100.0	447	AAE16448	E. amylov
7	128	100.0	447	ABO92226	Erwinia a
8	57	44.5	206	AAW29770	Malassezi
9	54	42.2	837	AAE12381	N-termina
10	54	42.2	837	AAE14656	Murine ST
11	54	42.2	837	ABU10480	Mouse STA
12	52	40.6	135	AAW56974	Partial P
13	52	40.6	135	AAW11979	Mycobacte
14	52	40.6	207	AAW61476	A. fumiga
15	52	40.6	210	ADM57310	Modular a
16	52	40.6	347	ADM57298	Modular a
17	49	38.3	110	ADK34437	Novel hum
18	49	38.3	164	ADJ25641	Voltage-g
19	49	38.3	436	ADN73559	Thale cre
20	49	38.3	613	ABR42419	Human pot
21	48.5	37.9	55	ABP02086	Human ORF
22	48.5	37.9	193	ADN99445	Novel hum
23	48.5	37.9	365	ABG60270	Human ova
24	48.5	37.9	365	ABG61741	Novel ova
25	48.5	37.9	392	ADM19994	Protein e

26	48	37.5	43	7	ADN59761	Adn59761 Peptide-v
27	48	37.5	238	5	ABP73460	Abp73460 Candida a
28	48	37.5	505	4	ABB58292	Abbs58292 Drosophil
29	47	36.7	72	7	ADF58708	Adf58708 Human pol
30	47	36.7	451	4	ABG10570	Abg10570 Novel hum
31	47	36.7	737	7	ADF83524	C. reinha
32	47	36.7	737	7	ADF83526	C. reinha
33	47	36.7	872	7	ADF83526	C. reinha
34	47	36.7	1343	6	AAU35444	Abu35444 Haemophil
35	47	36.7	1343	6	ABU30272	Abu30272 Protein e
36	47	36.7	1479	4	ABB70936	Abb70936 Drosophil
37	46.5	36.3	353	8	ADI43241	Adi43241 Plant tra
38	46.5	36.3	353	8	ADO62808	Ado62808 Transcrip
39	46.5	36.3	504	4	ABB66600	Abb66600 Drosophil
40	46	35.9	402	3	AAG06450	Aag06450 Arabidops
41	46	35.9	402	6	ADA33693	Ada33693 Acinetoba
42	46	35.9	403	3	AAG43157	Aag43157 Arabidops
43	46	35.9	408	4	AAB79473	Aab79473 Corynebac
44	46	35.9	419	7	ADB70132	C. neofor
45	46	35.9	434	3	AAG06449	Aag06449 Arabidops

## ALIGNMENTS

## RESULT 1

AAW96260  
ID AAW96260 standard; protein; 447 AA.

XX AAW96260;

DT 14-JUN-1999 (first entry)

DE Hypersensitive response eliciting protein (HrpW).

KW Hypersensitive response elicitor protein; hypersensitive response; hrpW;  
KW pathogen; infection; crop protection; disease resistance;  
KW pest resistance; transgenic plant; colouration; maturation.

OS Erwinia amylovora.

PN WO9907208-A1.

XX 18-FEB-1999.

PF 27-JUL-1998; 98WO-US015547.

PR 06-AUG-1997; 97US-0055108P.

XX (CORR ) CORNELL RES FOUND INC.

XX Kim JF, Beer SV;

DR WPI: 1999-167126/14.

DR N-PSDB; AAX09007.

XX New Erwinia amylovora hypersensitive response eliciting gene and protein  
PT - useful for providing transgenic plants and seeds with enhanced growth,  
PT and insect and disease resistance.

XX Claim 1; Page 50-51; 54pp; English.

XX The hypersensitive response eliciting protein (hrp) or polypeptide is  
XX produced as part of an active defense by plants against incompatible  
XX pathogen infections. The hypersensitive response is a rapid localised  
XX necrosis. The hrp protein and gene when used in nucleotide constructs are  
XX useful for providing disease resistance to plants, insect control to  
XX plants, and enhancing plant growth (enhancing fruit size and earlier  
XX colouration and maturation), by direct application of the protein to  
XX plants, or by producing transgenic plants or seeds using the hrp gene  
XX Sequence 447 AA;

```
Query Match      100.0%; Score 128; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPFLKAMLKLI A 25
DB 116 ITPDGGGGQIGDNPFLKAMLKLI A 140

RESULT 2
ID AAY71094 standard; protein; 447 AA.
XX
AC AAY71094;
XX
DT 08-SEP-2000 (first entry)
XX
DE Erwinia amylovora hypersensitive response elicitor #2.
XX
KW Hypersensitive response elicitor; environmental stress resistance; plant.
XX
OS Erwinia amylovora.
XX
PN WO200028055-A2.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026039.
XX
PR 05-NOV-1998; 98US-0107243P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Schading RL;
XX
DR WPI; 2000-376566/32.
XX
DR N-PSDB; AAD00669.
XX
PT Application of a hypersensitive response elicitor protein to plants to
PT impart stress resistance.
XX
PS Disclosure; Page 10-12; 84pp; English.
XX
SQ
XX The patent discloses a method to impart stress resistance to plants by
XX applying a hypersensitive response elicitor in a non-infectious form to a
XX plant or seed. The present sequence is a hypersensitive response elicitor
XX protein from Erwinia amylovora. The protein is heat stable, protease
XX sensitive and suppressed by inhibitors of plant metabolism. It is used to
XX impart stress resistance to plants
XX
SQ Sequence 447 AA;
Query Match      100.0%; Score 128; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPFLKAMLKLI A 25
DB 116 ITPDGGGGQIGDNPFLKAMLKLI A 140

RESULT 3
AAY84855
ID AAY84855 standard; protein; 447 AA.
XX
AC AAY84855;
XX
DT 08-AUG-2000 (first entry)
XX
DE A hypersensitive response elicitor protein.
XX
DE Hypersensitive response; insect control; disease resistance;
XX Hypersensitive response elicitor; plant growth; vegetable; crop;
KW
```

```
ornamental plant.
XX
OS Erwinia amylovora.
XX
PN WO200020452-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023181.
XX
PR 05-OCT-1998; 98US-0103050P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Fan H, Niggemeyer JL;
XX
DR WPI; 2000-303745/26.
XX
DR N-PSDB; AAA14939.
XX
PT Hypersensitive response elicitor polypeptides useful for imparting
PT enhanced growth, disease resistance and insect resistance to plants,
PT especially vegetables and ornamental flowers.
XX
PS Disclosure; Page 12-13; 100pp; English.
XX
SQ
XX The present sequence represents a hypersensitive response elicitor
XX polypeptide. The specification describes hypersensitive response elicitor
XX polypeptide fragments, which do not elicit a hypersensitive response.
XX Instead, the proteins impart disease resistance to plants, enhance plant
XX growth, and/or control insects. The polypeptide fragments may be used to
XX these properties to plants. The plants which may be treated in this way
XX include vegetables, crops and ornamental plants such as alfalfa, rice,
XX wheat, bean, pea, chickory, lettuce, endive, cabbage, brussel sprout,
XX beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion,
XX garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini,
XX cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry,
XX pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis
XX thaliana, saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum,
XX carnation or zinnia
XX
SQ Sequence 447 AA;
Query Match      100.0%; Score 128; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPFLKAMLKLI A 25
DB 116 ITPDGGGGQIGDNPFLKAMLKLI A 140

RESULT 4
AAO22548
ID AAO22548 standard; protein; 447 AA.
XX
AC AAO22548;
XX
DT 28-OCT-2002 (first entry)
XX
DE Hypersensitive response elicitor protein #2 from Erwinia amylovora.
XX
KW Desiccation inhibitor; longevity enhancer; desiccation inhibitor;
KW cutting; ornamental plant; hypersensitive response elicitor protein;
KW transgenic ornamental plant; early flowering; longevity enhancer; plant;
KW flower bloom; flower.
XX
OS Erwinia amylovora.
XX
PN WO200237960-A2.
XX
PD 16-MAY-2002.
XX
```

```

PF 06-NOV-2001; 2001WO-US043715.
XX
PR 13-NOV-2000; 2000US-0248169P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Leon E, Oviedo A;
XX
DR WPI; 2002-575194/61.
DR N-PSDB; AAL41133.
XX
PT Inhibiting desiccation of cuttings from ornamental plants, by treating
PT ornamental plants with hypersensitive response elicitor protein, or
PT expressing heterologous hypersensitive response elicitor protein in
PT plants.
XX
PS Disclosure; Page 12-13; 69pp; English.
XX
CC The invention relates to a method for inhibiting desiccation of cuttings
CC from ornamental plants. The method involves treating the cuttings with a
CC hypersensitive response elicitor protein or polypeptide, or providing a
CC transgenic ornamental plant or plant seed transformed with a DNA molecule
CC encoding the hypersensitive response elicitor polypeptide, and growing
CC the ornamental plant or transgenic ornamental plant produced from the
CC transgenic ornamental plant seed. The hypersensitive response elicitor
CC protein or polypeptide is useful for inhibiting desiccation of cuttings
CC from ornamental plants, for harvesting cuttings from ornamental plants,
CC for promoting early flowering of ornamental plants, and enhancing the
CC longevity of flower blooms on ornamental plant cuttings. This sequence
CC represents a hypersensitive response elicitor protein of the invention
XX
SQ Sequence 447 AA;

      Query Match      100.0%; Score 128; DB 5; Length 447;
      Best Local Similarity 100.0%; Pred. No. 5.9e-11;
      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKAMKLIA 25
   |||||
Db 116 ITPDGGGGGQIGDNPFLKAMKLIA 140
   |||||

RESULT 5
AAE18296
ID AAE18296 standard; protein; 447 AA.
XX
AC AAE18296;
XX
DT 07-MAY-2002 (first entry)
XX
DE Erwinia amylovora hypersensitive response elicitor (HRE) #2.
XX
KW Hypersensitive response elicitor; HRE; transgenic plant; plant growth;
KW stress tolerance; disease tolerance; modified flower colour;
KW insect resistance; herbicide resistance; male sterility.
XX
OS Erwinia amylovora.
XX
PN WO2001195724-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US018955.
XX
PR 15-JUN-2000; 2000US-0211585P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Derocher J;
XX
DR WPI; 2002-130707/17.
DR N-PSDB; AAD29125.
XX

      Query Match      100.0%; Score 128; DB 5; Length 447;
      Best Local Similarity 100.0%; Pred. No. 5.9e-11;
      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKAMKLIA 25
   |||||
Db 116 ITPDGGGGGQIGDNPFLKAMKLIA 140
   |||||

RESULT 6
AAE16448
ID AAE16448 standard; protein; 447 AA.
XX
AC AAE16448;
XX
DT 09-APR-2002 (first entry)
XX
DE E. amylovora hypersensitive response elicitor protein #2.
XX
KW Hypersensitive response elicitor protein; plant growth; fruit coloration;
KW disease resistance; stress resistance; phytotoxin; insect infection;
KW plant maturation.
XX
OS Erwinia amylovora.
XX
FH Key
XX
FT Domain 5..64
   /label= Hypersensitive_response_eliciting_domain_1
FT Region 5..45
   /label= Acidic_unit
FT Region 45..64
   /label= Alpha_helix
FT Domain 103..146
   /label= Hypersensitive_response_eliciting_domain_2
FT Region 103..131
   /label= Acidic_unit
FT Region 131..146
   /label= Alpha_helix
XX
PN WO200198501-A2.
XX
PD 27-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US018820.
XX
PR 16-JUN-2000; 2000US-0212211P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Fan H, Wei Z;
XX
DR WPI; 2002-122282/16.
DR N-PSDB; AAD27016.
XX

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```

PF 06-NOV-2001; 2001WO-US043715.
XX
PR 13-NOV-2000; 2000US-0248169P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Leon E, Oviedo A;
XX
DR WPI; 2002-575194/61.
DR N-PSDB; AAL41133.
XX
PT Inhibiting desiccation of cuttings from ornamental plants, by treating
PT ornamental plants with hypersensitive response elicitor protein, or
PT expressing heterologous hypersensitive response elicitor protein in
PT plants.
XX
PS Disclosure; Page 12-13; 69pp; English.
XX
CC The invention relates to a method for inhibiting desiccation of cuttings
CC from ornamental plants. The method involves treating the cuttings with a
CC hypersensitive response elicitor protein or polypeptide, or providing a
CC transgenic ornamental plant or plant seed transformed with a DNA molecule
CC encoding the hypersensitive response elicitor polypeptide, and growing
CC the ornamental plant or transgenic ornamental plant produced from the
CC transgenic ornamental plant seed. The hypersensitive response elicitor
CC protein or polypeptide is useful for inhibiting desiccation of cuttings
CC from ornamental plants, for harvesting cuttings from ornamental plants,
CC for promoting early flowering of ornamental plants, and enhancing the
CC longevity of flower blooms on ornamental plant cuttings. This sequence
CC represents a hypersensitive response elicitor protein of the invention
XX
SQ Sequence 447 AA;

      Query Match      100.0%; Score 128; DB 5; Length 447;
      Best Local Similarity 100.0%; Pred. No. 5.9e-11;
      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKAMKLIA 25
   |||||
Db 116 ITPDGGGGGQIGDNPFLKAMKLIA 140
   |||||

RESULT 5
AAE18296
ID AAE18296 standard; protein; 447 AA.
XX
AC AAE18296;
XX
DT 07-MAY-2002 (first entry)
XX
DE Erwinia amylovora hypersensitive response elicitor (HRE) #2.
XX
KW Hypersensitive response elicitor; HRE; transgenic plant; plant growth;
KW stress tolerance; disease tolerance; modified flower colour;
KW insect resistance; herbicide resistance; male sterility.
XX
OS Erwinia amylovora.
XX
PN WO2001195724-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US018955.
XX
PR 15-JUN-2000; 2000US-0211585P.
XX
PA (EDEN-) EDEN BIOSCIENCE CORP.
XX
PI Wei Z, Derocher J;
XX
DR WPI; 2002-130707/17.
DR N-PSDB; AAD29125.
XX

```

PT Phytophthora, or Erwinia) or desiccation and enhancing the longevity in a  
PT fruits or vegetables, using hypersensitive response elicitor proteins or  
PT nucleic acids.  
XX  
XX Disclosure; Page 11-12; 72pp; English.  
PS  
XX The present invention describes methods for inhibiting post harvest  
CC disease or desiccation and enhancing the longevity in a fruits or  
CC vegetables, using hypersensitive response elicitor proteins or  
CC polypeptides or nucleic acids (I) derived from pathogens (e.g. Erwinia  
CC amylovorae, E. stewartii, E. chrysanthemi, E. carotovora, Xanthomonas,  
CC pseudomonas syringae, P. solanacearum, Phytophthora, and Clavibacter).  
CC (I) has bactericidal activity, and can be used in gene therapy. The  
CC method can be used for inhibiting post harvest disease (caused by  
CC penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and  
CC enhancing the longevity in a fruits or vegetables. The method enables  
CC growers, warehouse packers, shippers and suppliers to process, handle and  
CC store fruit and vegetables with reduced losses caused by post harvest  
CC disease and desiccation, therefore reducing costs to the consumer and  
CC improving quality. The present sequence represents a hypersensitive  
CC response elicitor protein given in the exemplification of the present  
CC invention  
XX  
XX Sequence 447 AA;  
SQ  
Query Match 100.0%; Score 128; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 5.9e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ITPDGGGGGIGDNPPLKAMLKLI 25  
DB 116 ITPDGGGGGIGDNPPLKAMLKLI 140  
RESULT 8  
AAW29770  
ID AAW29770 standard; protein; 206 AA.  
XX  
XX AAW29770;  
XX  
XX 27-AUG-2003 (revised)  
DT 23-FEB-1998 (first entry)  
XX  
XX Malassezia fungus MP-3 antigenic protein.  
DE Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;  
XX  
XX allergy; antigen.  
XX  
XX Malassezia.  
OS  
XX  
XX WO9721817-A1.  
FN  
XX  
XX 19-JUN-1997.  
PD  
XX  
XX 10-DEC-1996; 96WO-JP003602.  
PF  
XX  
XX 12-DEC-1995; 95JP-00346627.  
PR  
XX  
XX 05-SEP-1996; 96JP-00257612.  
PR  
XX  
XX 05-SEP-1996; 96JP-00257613.  
PR  
XX  
XX (TAKI ) TAKARA SHUZO CO LTD.  
PA  
XX  
XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;  
PI Akiyama K, Yasueda H, Yamaguchi H;  
PI  
XX  
XX WPI; 1997-332788/30.  
DR  
XX  
XX N-PSDB; AAT85876.  
DR  
XX  
XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies  
PT present in patients with Malassezia allergies, useful for diagnosis,  
PT treatment and prevention of such conditions.  
XX  
XX Claim 36; Page 83-84; 162pp; Japanese.  
PS

XX New hypersensitive response elicitor proteins comprising spaced apart  
PT domains having an acidic portion linked to an alpha-helix, useful for  
PT imparting disease or stress resistance, controlling insects or enhancing  
PT plant growth.  
XX  
XX Disclosure; Page 13-14; 99pp; English.  
PS  
XX The patent discloses hypersensitive response elicitor proteins and  
CC nucleotides encoding such proteins. Hypersensitive response elicitor  
CC proteins comprise an isolated pair or more of spaced apart domains, each  
CC comprising an acidic portion linked to an alpha-helix and capable of  
CC eliciting a hypersensitive response in plants. Sequences of the invention  
CC are used to impart disease resistance to plants, to enhance plant growth,  
CC to control insects and/or to impart stress resistance to plants which  
CC includes resistance to environmental stresses such as climate, air  
CC pollution, chemical and nutritional stress. The method of imparting  
CC disease resistance has the potential for treating previously untreatable  
CC diseases, treating diseases systemically and avoiding the use of  
CC infectious agents or environmentally harmful materials. Hyper- sensitive  
CC response elicitor sequences are used to enhance plant growth which  
CC encompasses greater yield, increased in quantity of seeds produced,  
CC percentage of seeds germinated, plant size and biomass, bigger fruits,  
CC earlier fruit coloration and plant maturation. They are also used for  
CC insect control which encompasses preventing direct insect damage to plant  
CC by feeding injury, interfering with insect larval feeding on the plants,  
CC preventing insects from colonising host plants and releasing phytotoxins.  
CC Sequences of the invention also prevent subsequent disease damage to  
CC plants resulting from insect infection. The present sequence is Erwinia  
CC amylovorae hypersensitive response elicitor protein  
XX  
XX Sequence 447 AA;  
SQ  
Query Match 100.0%; Score 128; DB 5; Length 447;  
Best Local Similarity 100.0%; Pred. No. 5.9e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ITPDGGGGGIGDNPPLKAMLKLI 25  
DB 116 ITPDGGGGGIGDNPPLKAMLKLI 140  
RESULT 7  
ABB09226  
ID ABB09226 standard; protein; 447 AA.  
XX  
XX ABB09226;  
AC  
XX  
XX 08-JUL-2002 (first entry)  
DT  
XX  
XX Erwinia amylovorae hypersensitive response elicitor SEQ ID NO:5.  
DE  
XX  
XX Hypersensitive response elicitor; fruit; vegetable; plant; desiccation;  
XX postharvest disease.  
KW  
XX  
XX Erwinia amylovorae.  
OS  
XX  
XX WO200180639-A2.  
FN  
XX  
XX 01-NOV-2001.  
PD  
XX  
XX 17-APR-2001; 2001WO-US012468.  
PF  
XX  
XX 19-APR-2000; 2000US-0198359P.  
PR  
XX  
XX (EDEN-) EDEN BIOSCIENCE CORP.  
FA  
XX  
XX Wei Z, Qiu D, Remick D;  
PI  
XX  
XX WPI; 2002-041357/05.  
DR  
XX  
XX N-PSDB; ABL51711.  
DR  
XX  
XX Inhibiting post harvest disease (caused by Penicillium, Botrytis,  
PT



The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT6 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal.

every Match 44.5%; Score 57; DB 2; Length 206;

Sequence	Conservative	Mismatches	Indels	Gaps
1	9	5	6	0
2	9	5	6	0
3	9	5	6	0
4	9	5	6	0
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6	9	5	6	0
7	9	5	6	0
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9	9	5	6	0
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13	9	5	6	0
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27	9	5	6	0
28	9	5	6	0
29	9	5	6	0
30	9	5	6	0
31	9	5	6	0
32	9	5	6	0
33	9	5	6	0
34	9	5	6	0
35	9	5	6	0
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1 ITPDGOGGGOIGDNPFLKAM 20

9  
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AAB12381:

08-NOV-2000 (first entry)

N-terminal domain of murine STAT-6 protein.

STAT: signal transducer and activator of transcription: crystal:

Mus sp.

Key	Location/Qualifiers
1	1
2	2
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region
4.9
/label= Alpha helix 1

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Region	11. .18	/label = Alpha bolix 3

Region

Region	31. .36	32. .37	33. .38	34. .39	35. .40	36. .41	37. .42	38. .43	39. .44	40. .45	41. .46	42. .47	43. .48	44. .49	45. .50	46. .51	47. .52	48. .53	49. .54	50. .55	51. .56	52. .57	53. .58	54. .59	55. .60	56. .61	57. .62	58. .63	59. .64	60. .65	61. .66	62. .67	63. .68	64. .69	65. .70	66. .71	67. .72	68. .73	69. .74	70. .75	71. .76	72. .77	73. .78	74. .79	75. .80	76. .81	77. .82	78. .83	79. .84	80. .85	81. .86	82. .87	83. .88	84. .89	85. .90	86. .91	87. .92	88. .93	89. .94	90. .95	91. .96	92. .97	93. .98	94. .99	95. .00	96. .01	97. .02	98. .03	99. .04	00. .05	01. .06	02. .07	03. .08	04. .09	05. .10	06. .11	07. .12	08. .13	09. .14	10. .15	11. .16	12. .17	13. .18	14. .19	15. .20	16. .21	17. .22	18. .23	19. .24	20. .25	21. .26	22. .27	23. .28	24. .29	25. .30	26. .31	27. .32	28. .33	29. .34	30. .35	31. .36	32. .37	33. .38	34. .39	35. .40	36. .41	37. .42	38. .43	39. .44	40. .45	41. .46	42. .47	43. .48	44. .49	45. .50	46. .51	47. .52	48. .53	49. .54	50. .55	51. .56	52. .57	53. .58	54. .59	55. .60	56. .61	57. .62	58. .63	59. .64	60. .65	61. .66	62. .67	63. .68	64. .69	65. .70	66. .71	67. .72	68. .73	69. .74	70. .75	71. .76	72. .77	73. .78	74. .79	75. .80	76. .81	77. .82	78. .83	79. .84	80. .85	81. .86	82. .87	83. .88	84. .89	85. .90	86. .91	87. .92	88. .93	89. .94	90. .95	91. .96	92. .97	93. .98	94. .99	95. .00	96. .01	97. .02	98. .03	99. .04	00. .05	01. .06	02. .07	03. .08	04. .09	05. .10	06. .11	07. .12	08. .13	09. .14	10. .15	11. .16	12. .17	13. .18	14. .19	15. .20	16. .21	17. .22	18. .23	19. .24	20. .25	21. .26	22. .27	23. .28	24. .29	25. .30	26. .31	27. .32	28. .33	29. .34	30. .35	31. .36	32. .37	33. .38	34. .39	35. .40	36. .41	37. .42	38. .43	39. .44	40. .45	41. .46	42. .47	43. .48	44. .49	45. .50	46. .51	47. .52	48. .53	49. .54	50. .55	51. .56	52. .57	53. .58	54. .59	55. .60	56. .61	57. .62	58. .63	59. .64	60. .65	61. .66	62. .67	63. .68	64. .69	65. .70	66. .71	67. .72	68. .73	69. .74	70. .75	71. .76	72. .77	73. .78	74. .79	75. .80	76. .81	77. .82	78. .83	79. .84	80. .85	81. .86	82. .87	83. .88	84. .89	85. .90	86. .91	87. .92	88. .93	89. .94	90. .95	91. .96	92. .97	93. .98	94. .99	95. .00	96. .01	97. .02	98. .03	99. .04	00. .05	01. .06	02. .07	03. .08	04. .09	05. .10	06. .11	07. .12	08. .13	09. .14	10. .15	11. .16	12. .17	13. .18	14. .19	15. .20	16. .21	17. .22	18. .23	19. .24	20. .25	21. .26	22. .27	23. .28	24. .29	25. .30	26. .31	27. .32	28. .33	29. .34	30. .35	31. .36	32. .37	33. .38	34. .39	35. .40	36. .41	37. .42	38. .43	39. .44	40. .45	41. .46	42. .47	43. .48	44. .49	45. .50	46. .51	47. .52	48. .53	49. .54	50. .55	51. .56	52. .57	53. .58	54. .59	55. .60	56. .61	57. .62	58. .63	59. .64	60. .65	61. .66	62. .67	63. .68	64. .69	65. .70	66. .71	67. .72	68. .73	69. .74	70. .75</
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Region	39.43
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Region	50.73
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Region	75. .90
Lower-alpha helix	

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93.  .113
/label= Alpha helix /

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/label= Alpha helix 8
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US6087478-A.

11-JUL-2000.

23-JAN-1998; 98US-00012710.

23-JAN-1998; 98US-00012710.

(ITYRO ) INTV ROCKFEETLER

Vinkemeier II      Moarafi I      Darnell JE      Kurjvan J.

WDT: 2000-EO5108/AF

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drug screening and development.

Disclosure; Fig 1; 42pp; English.

CC drugs. An antagonist of STAT N-terminal dimeric interactions that  
 CC inhibits the binding of the STAT dimers to adjacent weak binding sites on  
 CC a promoter of a gene, could be useful as drugs in the treatment of  
 CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other  
 CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,  
 CC can be used as drugs in the treatment of diseases e.g. anaemia,  
 CC neutropenia, thrombocytopenia, cancer, obesity, viral diseases and  
 CC growth retardation. The present sequence is murine STAT6 protein  
 XX  
 XX Sequence 837 AA;

Query Match 42.2%; Score 54; DB 5; Length 837;  
 Best Local Similarity 64.3%; Pred. No. 30;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGGGGIGDNPPLK 18  
 | : | | | : | | | |  
 Db 802 GGGGSLGSQPLK 815

RESULT 11  
 ABU10480  
 ID ABU10480 standard; protein; 837 AA.  
 XX  
 AC ABU10480;  
 DT 06-AUG-2003 (first entry)  
 XX  
 DE Mouse STAT6 protein.  
 XX  
 KW Mouse; signal transducer and activator of transcription; drug design;  
 KW drug screening; STAT-STAT dimer interaction; STAT6.  
 XX  
 OS Mus sp.

Key Location/Qualifiers  
 Region 4..9  
 /label= alpha\_helix\_1  
 Region 11..18  
 /label= alpha\_helix\_2  
 Region 24..29  
 /label= alpha\_helix\_3  
 Region 31..36  
 /label= alpha\_helix\_4  
 Region 39..43  
 /label= alpha\_helix\_5  
 Region 50..73  
 /label= alpha\_helix\_6  
 /note= "Residues 57, 61, 65, 68 and 71 contribute to  
 packing of the coiled-coil"  
 Region 75..90  
 /label= alpha\_helix\_7  
 /note= "Residues 77, 81, 84 and 88 contribute to packing  
 of the coiled-coil"  
 Region 93..113  
 /label= alpha\_helix\_8

US2003003563-A1.  
 02-JAN-2003.  
 19-OCT-2001; 2001US-00045792.  
 23-JAN-1998; 98US-00012710.  
 24-APR-2000; 2000US-00556273.  
 (VINK/) VINKEMEIER U.  
 (MOAR/) MOAREFI I.  
 (DARN/) DARNELL J E.  
 (KURI/) KURIYAN J.  
 Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

DR WPI; 2003-447354/42.  
 XX New crystal having an N-terminal domain of a STAT protein performing X-  
 PT ray crystallographic studies, useful for screening drugs that enhance or  
 PT inhibit STAT-STAT dimer interactions.  
 XX  
 PS Disclosure; Page 33-35; 46pp; English.  
 XX  
 CC The invention relates to a crystal of an N-terminal domain of signal  
 CC transducer and activator of transcription (STAT) protein, where the  
 CC crystal effectively diffracts X-rays for the determination of the atomic  
 CC coordinates of the N-terminal domain of the STAT protein to a resolution  
 CC of greater than 5.0 Angstrom. The methods and compositions are useful for  
 CC the design and screening of drugs that enhance or inhibit STAT-STAT dimer  
 CC interactions. The present sequence represents the amino acid sequence of  
 CC mouse STAT6 protein  
 XX  
 XX Sequence 837 AA;

Query Match 42.2%; Score 54; DB 6; Length 837;  
 Best Local Similarity 64.3%; Pred. No. 30;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGGGGIGDNPPLK 18  
 | : | | | : | | | |  
 Db 802 GGGGSLGSQPLK 815

RESULT 12  
 AAR56974  
 ID AAR56974 standard; protein; 135 AA.  
 XX  
 AC AAR56974;  
 DT 28-FEB-1995 (first entry)  
 XX  
 DE Partial PMGA 1.3 protein of Mycoplasma gallisepticum.  
 XX  
 KW PMGA; adhesin gene complex; hemagglutinin; conserved sequences; primers;  
 KW probes; amplification; polymerase chain reaction; specific; detection;  
 XX PCR; 1.2; 1.3.

Key Location/Qualifiers  
 Region 1..25  
 /label= putative signal peptide  
 Region 26..135  
 /label= mature pMGAL.2 protein

AU9350593-A.  
 26-MAY-1994.  
 10-NOV-1993; 93AU-00050593.  
 10-NOV-1992; 92AU-00005744.

(UYME ) UNIV MELBOURNE.  
 Browning GF, Markham PF, Whithear KG, Walker ID, Glew MD;  
 WPI; 1994-209061/26.  
 N-PSDB; AAQ68668.

Recombinant DNA constructs for Mycoplasma gallisepticum - for diagnosis,  
 treatment and prophylaxis of poultry respiratory disorders.  
 Example 1; Fig 3; 51pp; English.

AAR56974 shows the partial amino acid sequence of pMGAL.3 derived from  
 the partial DNA sequence of a 10 kb insert from a Mycoplasma  
 gallisepticum genomic DNA library, detected by probes based on the T3 and

CC C7 peptides. The proteins derived show high homology to pMGA. This  
 CC sequence is the best approximation of the sequence given in the  
 CC specification due to poor print quality. Mycoplasma gallisepticum  
 CC infection in poultry, humans and other animals is of economic importance  
 CC to many industries and it is desirable to produce effective vaccines and  
 CC probes for its detection. The sequences and probes and vaccine vectors of  
 CC the invention can be used for the diagnosis and treatment of Mycoplasma  
 CC gallisepticum infection, and for prophylaxis

XX SQ Sequence 135 AA;  
 Query Match 40.6%; Score 52; DB 2; Length 135;  
 Best Local Similarity 64.3%; Pred. No. 7.8;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TPDGGGGGQIGDNP 15  
 DB 57 TNPNGGGGMMGDNP 70

RESULT 13  
 AAW11979  
 ID AAW11979 standard; protein; 135 AA.  
 XX AC AAW11979;  
 XX DT 16-OCT-2003 (revised)  
 DT 23-APR-1997 (first entry)  
 XX DE Mycobacterium gallisepticum pMGA1.3 adhesin partial sequence.  
 XX KW Adhesin; pMGA; mycoplasma; diagnosis; vaccine; vector;  
 KW respiratory disease; poultry; haemagglutinin.  
 XX OS Mycoplasma gallisepticum; strain S6.  
 XX FH Key Location/Qualifiers  
 FT Peptide  
 FT 1..25  
 FT /label= Sig\_peptide  
 FT /note= "the signal peptide shows homology to the pMGA1.2  
 FT signal peptide"

CA2135330-A.  
 11-MAY-1995.  
 08-NOV-1994; 94CA-02135330.  
 10-NOV-1993; 93AU-00050593.  
 20-APR-1994; 94US-00230312.  
 (BROW/) BROWNING G F.  
 Browning GF, Markham PF, Whithear KG, Walker ID, Glew MD;  
 WPI; 1995-241027/32.  
 N-PSDB; AAT51531.  
 New promoter region from a Mycoplasma gallisepticum adhesin gene - useful  
 when coupled to foreign antigen gene, for prodn. of multivalent live  
 vaccines, also new probes for detecting Mycoplasma and manipulating its  
 genome.

Discloure; Fig 3; 81pp; English.

Adhesin pMGA1.2 (AAW11978) and adhesin pMGA1.3 fragment (AAW11979) are  
 products of gene sequences (see also AAT51531) isolated from Mycoplasma  
 gallisepticum. DNA constructs incorporating the promoter and/or signal  
 sequences of the pMGA genes can be used in the prodn. of multivalent live  
 vaccines. The signal peptide sequence is utilised where attachment of an  
 exogenous antigen gene to the mycoplasma cell membrane is required.  
 (Updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 135 AA;  
 Query Match 40.6%; Score 52; DB 2; Length 135;  
 Best Local Similarity 64.3%; Pred. No. 7.8;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TPDGGGGGQIGDNP 15  
 DB 57 TNPNGGGGMMGDNP 70

RESULT 14  
 AAW61476  
 ID AAW61476 standard; protein; 207 AA.  
 XX AC AAW61476;  
 XX DT 19-OCT-1998 (first entry)  
 XX DE A. fumigatus allergen rAsp f6 sequence.  
 KW Aspergillus fumigatus; allergic bronchopulmonary aspergillosis; allergen;  
 KW rAsp f6; human; ABPA; asthma; cystic fibrosis.  
 XX OS Aspergillus fumigatus.  
 XX PN WO9828624-A1.  
 XX PD 02-JUL-1998.  
 XX PF 19-DEC-1997; 97WO-SE002172.  
 XX PR 20-DEC-1996; 96SE-00004815.  
 XX PA (PHAA ) PHARMACIA & UPJOHN DIAGNOSTICS AB.  
 XX PI Cramer R, Hemmann S, Blaser K;  
 XX DR WPI; 1998-377789/32.  
 XX N-PSDB; AAV45115.  
 DR Method for diagnosing allergic broncho-pulmonary aspergillosis - by  
 PT determining if individual carries antibodies reactive with one or more  
 PT ABPA-related recombinant allergens.  
 XX PS Disclosure; Page 34; 42pp; English.  
 XX CC This represents an Aspergillus fumigatus allergen rAsp f6. The allergens  
 CC rAsp f6, rAsp f4 and rAsp f8 are non-secreted proteins from A. fumigatus  
 CC and are related to allergic bronchopulmonary aspergillosis (ABPA). The  
 CC invention provides a method for diagnosing ABPA in a human individual,  
 CC characterised by determining if the individual carries antibodies  
 CC reactive with one or more ABPA-related recombinant antigens. The method  
 CC can be used to detect ABPA in a patient and differentiate from allergic  
 CC sensitisation to Aspergillus fumigatus, particularly in patients  
 CC suffering from asthma or cystic fibrosis

SQ Sequence 207 AA;  
 Query Match 40.6%; Score 52; DB 2; Length 207;  
 Best Local Similarity 40.9%; Pred. No. 13;  
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKAWLK 22  
 DB 81 LAPEKSGGGKIDQAPVLKAAIE 102

RESULT 15  
 ADM57310  
 ID ADM57310 standard; protein; 210 AA.  
 XX AC ADM57310;

Query Match 40.6%; Score 52; DB 8; Length 210;  
Best Local Similarity 40.9%; Pred. No. 13;  
Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Search completed: January 25, 2005, 20:30:27  
Job time : 45.9904 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 20:14:24 ; Search time 18.2692 Seconds  
(without alignments)  
90.751 Million cell updates/sec

Title: DESAI-879\_116\_140  
Perfect score: 128  
Sequence: 1 ITPDQGGGQIGDNPFLKAMKLIA 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	447	3	US-09-120-927-2
2	128	100.0	447	4	US-09-431-614-6
3	57	44.5	206	4	US-09-091-097-6
4	54	42.2	837	3	US-09-012-710-12
5	54	42.2	837	3	US-09-556-273-12
6	51	39.8	409	3	US-09-140-466-3
7	48	37.5	252	4	US-09-248-796A-18831
8	48	37.5	256	4	US-09-270-767-46260
9	47	36.7	379	2	US-08-576-626A-50
10	46	35.9	402	4	US-09-328-352-4980
11	46	35.9	502	4	US-09-270-767-45060
12	46	35.9	749	2	US-08-568-459A-6
13	46	35.9	749	2	US-08-487-826B-6
14	46	35.9	749	3	US-09-210-288-6
15	46	35.9	1098	4	US-09-252-991A-20186
16	45	35.2	82	4	US-09-248-796A-22679
17	45	35.2	133	4	US-09-543-681A-6484
18	45	35.2	230	4	US-09-270-767-39647
19	45	35.2	230	4	US-09-270-767-54864
20	45	35.2	365	3	US-09-151-592-2
21	45	35.2	365	3	US-09-254-077A-10
22	45	35.2	365	4	US-09-443-766-13
23	45	35.2	373	3	US-09-254-077A-12
24	45	35.2	427	4	US-09-270-767-42751
25	45	35.2	515	2	US-08-705-660-46
26	45	35.2	515	3	US-08-989-045-45
27	45	35.2	664	4	US-09-538-092-838

28	45	35.2	1403	4	US-09-252-991A-25500	Sequence 25500, A
29	44.5	34.8	1151	4	US-09-328-352-5876	Sequence 5876, Ap
30	44	34.4	335	4	US-09-252-991A-24116	Sequence 24116, A
31	44	34.4	399	4	US-09-489-039A-14312	Sequence 14312, A
32	44	34.4	690	4	US-09-248-796A-19169	Sequence 19169, A
33	44	34.4	816	4	US-09-540-236-3443	Sequence 3443, Ap
34	43.5	34.0	149	3	US-09-227-357-136	Sequence 196, Appl
35	43.5	34.0	415	3	US-09-100-193-2	Sequence 2, Appl
36	43	33.6	359	4	US-09-252-991A-18134	Sequence 18134, A
37	43	33.6	450	4	US-09-252-991A-27345	Sequence 27345, A
38	43	33.6	515	4	US-09-252-991A-32251	Sequence 32251, A
39	43	33.6	619	4	US-09-252-991A-32940	Sequence 32940, A
40	43	33.6	706	4	US-09-270-767-40994	Sequence 40994, A
41	43	33.6	706	4	US-09-270-767-56210	Sequence 56210, A
42	43	33.6	975	4	US-09-328-352-4764	Sequence 4764, Ap
43	42.5	33.2	197	4	US-09-270-767-32061	Sequence 32061, A
44	42.5	33.2	197	4	US-09-270-767-47278	Sequence 47278, A
45	42.5	33.2	262	4	US-09-248-796A-19720	Sequence 19720, A

## ALIGNMENTS

RESULT 1  
US-09-120-927-2  
; Sequence 2, Application US/09120927  
; Patent No. 6262018  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jihyun Francis  
; APPLICANT: Beer, Steven V  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM  
; TITLE OF INVENTION: ERYTHROCYTE AMYLOVORA AND ITS USE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hartgrave, Devans & Doyle LLP  
; STREET: P O Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,927  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/055,108  
; FILING DATE: 06-AUG-1977  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1581  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-120-927-2

Query Match 100.0%; Score 128; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ITPDQGGGQIGDNPFLKAMKLIA 25

Wed Jan 26 08:08:24 2005

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;
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-091-097-6

Query Match 44.5%; Score 57; DB 4; Length 206;
Best Local Similarity 45.0%; Pred. No. 0.6;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPPLKAM 20
Db 86 LAPQSGGGQLNDGPLKQAI 105

RESULT 4
US-09-012-710-12
; Sequence 12, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-012-710-12

Query Match 42.2%; Score 54; DB 3; Length 837;
Best Local Similarity 64.3%; Pred. No. 8.1;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGGGQIGDNPPLK 18
Db 802 GEGGSLGSQPLK 815

;
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-091-097-6

Query Match 100.0%; Score 128; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPPLKAMKLIA 25
Db 116 ITPDGGGGQIGDNPPLKAMKLIA 140

RESULT 3
US-09-091-097-6
; Sequence 6, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
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RESULT 5  
US-09-556-273-12  
; Sequence 12, Application US/09556273  
; Patent No. 6312887  
; GENERAL INFORMATION:  
; APPLICANT: Vinkemeier, Uwe  
; APPLICANT: Moarefi, Ismail  
; APPLICANT: Darnell, Jr., James E.  
; APPLICANT: Kuriyan, John  
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A  
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue, 4th Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/556,273  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 09/012,710  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-194  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 837 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-09-556-273-12

Query Match 42.2%; Score 54; DB 3; Length 837;  
Best Local Similarity 64.3%; Pred. No. 8.1;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 5 GGGGGQIGDNPILK 18  
DB 802 GGGGSLGSQPLK 815

RESULT 6  
US-09-140-466-3  
; Sequence 3, Application US/09140466  
; Patent No. 6268160  
; GENERAL INFORMATION:  
; APPLICANT: CLOUGH, BARBARA  
; APPLICANT: PREISER, PETER  
; APPLICANT: WILSON, ROBERT  
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE  
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS  
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS  
; FILE REFERENCE: N68837B GCW RJC DP  
; CURRENT APPLICATION NUMBER: US/09/140,466  
; CURRENT FILING DATE: 1998-08-26

; EARLIER APPLICATION NUMBER: US 60/056,246  
; EARLIER FILING DATE: 1997-08-28  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Anacystis nidulans  
US-09-140-466-3

Query Match 39.8%; Score 51; DB 3; Length 409;  
Best Local Similarity 57.1%; Pred. No. 10;  
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;  
QY 6 QCG--GQIGDNPILKAMKLI 24  
DB 183 QCGASGQKGDNPWDKILKLM 203

RESULT 7  
US-09-248-796A-18831  
; Sequence 18831, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18831  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18831

Query Match 37.5%; Score 48; DB 4; Length 252;  
Best Local Similarity 43.5%; Pred. No. 17;  
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
QY 2 TPDGGGGQIGDNPILKAMKLI 24  
DB 64 TTDGNGGGGIGIVPTLQIVATV 86

RESULT 8  
US-09-270-767-46260  
; Sequence 46260, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 46260  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-46260

Query Match 37.5%; Score 48; DB 4; Length 256;  
Best Local Similarity 47.6%; Pred. No. 18;  
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;  
QY 4 DQGGGGQIGDNPILKAMKLI 24

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DB      40 DGDGGDGGGEVTLAKMSLL 60
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40 DGDGGDGGGEVTLAKMSLL 60

RESULT 9
US-08-576-626A-50
; Sequence 50, Application US/08576626A
; Patent No. 5998194
; GENERAL INFORMATION:
; APPLICANT: Summers, R.G.
; APPLICANT: Katz, L.
; APPLICANT: Donadio, S.
; APPLICANT: Staver, M.J.
; TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
; TITLE OF INVENTION: BIOSYNTHESIS GENES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/576,626A
; FILING DATE: 21-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane Casulo
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 5857.US.O1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 938-3137
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-576-626A-50

Query Match 36.7%; Score 47; DB 2; Length 379;
Best Local Similarity 56.2%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ITPDGGGQIGDNPL 16
Db 189 ITS GGEGGAVITDNPFV 204

RESULT 10
US-09-328-352-4980
; Sequence 4980, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bregon et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
;
US-08-568-459A-6

Query Match 35.9%; Score 46; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 TPDGGGGGQIGDNPLLK 18
Db 432 TPNSSGGGNYGDRQISK 448

RESULT 14
US-09-210-288-6
; Sequence 6, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
;
US-09-210-288-6

Query Match 35.9%; Score 46; DB 3; Length 749;
Best Local Similarity 47.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 TPDGGGGGQIGDNPLLK 18
Db 432 TPNSSGGGNYGDRQISK 448

RESULT 15
US-09-210-288-6

Query Match 35.9%; Score 46; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 TPDGGGGGQIGDNPLLK 18
Db 432 TPNSSGGGNYGDRQISK 448

RESULT 14
US-08-487-826B-6
; Sequence 6, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-252-991A-20186  
; Sequence 20186, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20186  
; LENGTH: 1098  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20186

Query Match 35.9%; Score 46; DB 4; Length 1098;  
Best Local Similarity 47.6%; Pred. No. 1.8e+02;  
Matches 10; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 1 ITPDGGGGGQ---IGDNPLL 17  
:|||||:|:|  
Db 594 VQPDGGGGAQRHRAGEGPHL 614

Search completed: January 25, 2005, 20:38:21  
Job time : 19.2692 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 20:37:16 ; Search time 60.3365 Seconds  
(without alignments)  
149.698 Million cell updates/sec

Title: DESAI-879\_116\_140

Perfect score: 128

Sequence: 1 ITPDQGGGGQIGDNPFLKAMKLIA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	100.0	447	9	US-09-835-684-5
2	128	100.0	447	9	US-09-880-371-5
3	128	100.0	447	9	US-09-879-248-6
4	128	100.0	447	14	US-10-010-390-5
5	128	100.0	447	15	US-10-441-736-6
6	128	100.0	447	17	US-10-847-142-5
7	57	44.5	206	14	US-10-103-670-10
8	54	42.2	837	14	US-10-045-792-12
9	51	39.8	409	9	US-09-845-335-3
10	50	39.1	78	15	US-10-424-599-214915
11	50	39.1	177	16	US-10-437-963-149121
12	49	38.3	149	17	US-10-425-115-231795
13	49	38.3	483	14	US-10-369-493-3880

14	48.5	37.9	365	9	US-09-908-711-100	Sequence 100, App
15	48	37.5	43	14	US-10-269-806-163	Sequence 163, App
16	48	37.5	111	16	US-10-437-963-124136	Sequence 124136, App
17	48	37.5	238	14	US-10-032-585-7297	Sequence 7297, App
18	47.5	37.1	207	17	US-10-425-115-301902	Sequence 301902, App
19	47	36.7	81	17	US-10-425-115-347563	Sequence 347563, App
20	47	36.7	102	15	US-10-424-599-216781	Sequence 216781, App
21	47	36.7	134	17	US-10-425-115-351040	Sequence 351040, App
22	47	36.7	213	17	US-10-425-115-210287	Sequence 210287, App
23	47	36.7	435	14	US-10-369-493-6514	Sequence 6514, App
24	47	36.7	1343	9	US-09-815-242-11037	Sequence 11037, App
25	47	36.7	1343	15	US-10-282-122A-58196	Sequence 58196, App
26	46.5	36.3	353	15	US-10-374-780A-1704	Sequence 1704, App
27	46.5	36.3	353	16	US-10-437-963-194124	Sequence 194124, App
28	46.5	36.3	354	16	US-10-437-963-195060	Sequence 195060, App
29	46	35.9	408	16	US-10-781-014-462	Sequence 462, App
30	46	35.9	419	15	US-10-320-797-3176	Sequence 3176, App
31	46	35.9	441	9	US-09-738-626-5914	Sequence 5914, App
32	46	35.9	450	17	US-10-425-115-332466	Sequence 332466, App
33	46	35.9	469	15	US-10-425-114-57241	Sequence 57241, App
34	46	35.9	749	13	US-10-153-273-6	Sequence 6, Appl
35	46	35.9	1086	9	US-09-924-154-15	Sequence 15, Appl
36	45.5	35.5	113	15	US-10-424-599-183658	Sequence 183658, App
37	45.5	35.5	161	14	US-10-369-493-5035	Sequence 5035, App
38	45.5	35.5	880	16	US-10-437-963-119573	Sequence 119573, App
39	45	35.2	23	14	US-10-269-806-176	Sequence 176, App
40	45	35.2	41	14	US-10-269-806-170	Sequence 170, App
41	45	35.2	46	14	US-10-269-806-182	Sequence 182, App
42	45	35.2	46	14	US-10-269-806-188	Sequence 188, App
43	45	35.2	69	16	US-10-437-963-128768	Sequence 128768, App
44	45	35.2	79	17	US-10-425-115-333561	Sequence 333561, App
45	45	35.2	104	17	US-10-425-115-239179	Sequence 239179, App

#### ALIGNMENTS

##### RESULT 1

US-09-835-684-5  
; Sequence 5, Application US/09835684  
; Patent No. US20020019337A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Qiu, Dewen  
; TITLE OF INVENTION: Remick, Dean  
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR DESICCATION  
; TITLE OF INVENTION: DESICCATION  
; FILE REFERENCE: 21829/71  
; CURRENT APPLICATION NUMBER: US/09/835,684  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/198,359  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
US-09-835-684-5

Query Match 100.0%; Score 128; DB 9; Length 447;  
Best Local Similarity 100.0%; Pred. No. 3e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ITPDQGGGGQIGDNPFLKAMKLIA 25

Db 116 ITPDQGGGGQIGDNPFLKAMKLIA 140

##### RESULT 2

US-09-880-371-5  
; Sequence 5, Application US/09880371

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; Patent No. US2002005958A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: DeRoche, Jay
; TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 21829/91
; CURRENT APPLICATION NUMBER: US/09/880,371
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,585
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-09-880-371-5

Query Match 100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

RESULT 3
US-09-879-248-6
; Sequence 6, Application US/09879248
; Patent No. US20020062500A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Hao
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21829/81
; CURRENT APPLICATION NUMBER: US/09/879,248
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/212,211
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-09-879-248-6

Query Match 100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

RESULT 4
US-10-010-390-5
; Sequence 5, Application US/10010390
; Publication No. US20030104979A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Leon, Ernesto
; APPLICANT: Oviedo, Agustín
; TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
; TITLE OF INVENTION: FROM ORNAMENTAL PLANTS
; FILE REFERENCE: 21829/111
; CURRENT APPLICATION NUMBER: US/10/010,390
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/248,169
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-10-010-390-5

Query Match 100.0%; Score 128; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

RESULT 5
US-10-441-736-6
; Sequence 6, Application US/10441736
; Publication No. US20040016029A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Schading, Richard L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/203 (EBC-003)
; CURRENT APPLICATION NUMBER: US/10/441,736
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/107,243
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/431,614
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-10-441-736-6

Query Match 100.0%; Score 128; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

RESULT 6
US-10-847-142-5
; Sequence 5, Application US/10847142
; Publication No. US20040265442A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Qiu, Dewen
; APPLICANT: Renick, Dean
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
; TITLE OF INVENTION: DESICCATION
; FILE REFERENCE: 21829/197
; CURRENT APPLICATION NUMBER: US/10/847,142
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/198,359
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/835,684
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-10-847-142-5

Query Match 100.0%; Score 128; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

RESULT 6
US-10-847-142-5
; Sequence 5, Application US/10847142
; Publication No. US20040265442A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Qiu, Dewen
; APPLICANT: Renick, Dean
; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
; TITLE OF INVENTION: DESICCATION
; FILE REFERENCE: 21829/197
; CURRENT APPLICATION NUMBER: US/10/847,142
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/198,359
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/835,684
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-10-847-142-5

Query Match 100.0%; Score 128; DB 15; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPLKAMKLLIA 25
Db 116 ITPDGGGGGQIGDNPLKAMKLLIA 140

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; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-10-847-142-5

Query Match      100.0%; Score 128; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-10; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 ITPDGGGGQIGDNPFLKAMLKLI 25
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Db 116 ITPDGGGGQIGDNPFLKAMLKLI 140

RESULT 7
US-10-109-670-10
; Sequence 10, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 10
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-10

Query Match      44.5%; Score 57; DB 14; Length 206;
Best Local Similarity 45.0%; Pred. No. 3.4;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPFLKAM 20
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Db 86 LAPQSEGGQLNDGPKQAI 105

RESULT 8
US-10-045-792-12
; Sequence 12, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; Moarefi, Ismail
; Darnell, Jr., James E.
; Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
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; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-045-792-12

Query Match      42.2%; Score 54; DB 14; Length 837;
Best Local Similarity 64.3%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGGGGQIGDNPFLK 18
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Db 802 GEGGSLGSGQPLK 815

RESULT 9
US-09-845-335-3
; Sequence 3, Application US/09845335
; Patent No. US20020058266A1
; GENERAL INFORMATION:
; APPLICANT: CLOUGH, BARBARA
; APPLICANT: PREISER, PETER
; APPLICANT: WILSON, ROBERT
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
; FILE REFERENCE: N68837B GCW PJC DP
; CURRENT APPLICATION NUMBER: US/09/845,335
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/140,466
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Anacystis nidulans
US-09-845-335-3

Query Match      39.8%; Score 51; DB 9; Length 409;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 6 QGG--GQIGDNPFLKAMLKLI 24
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Db 183 QGGASGQKGDNPWVDKILKLM 203

RESULT 10
US-10-424-599-214915
; Sequence 214915, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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Wed Jan 26 08:08:25 2005

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; NAME/KEY: unsure
; LOCATION: (1)-(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_142992C.1.pap
US-10-425-115-231795

Query Match      38.3%; Score 49; DB 17; Length 149;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 PDGGGGGQIGDN 14
      |||:|||||:
Db      65 PDGEGGGQTDD 76

RESULT 13
US-10-369-493-3880
; Sequence 3880, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3880
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3880

Query Match      38.3%; Score 49; DB 14; Length 483;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      3 PDGGGGGQIGDNPLK 18
      |||:|||||:
Db      420 PEGGGSRDGDVLMK 435

RESULT 14
US-09-908-711-100
; Sequence 100, Application US/09908711
; Patent No. US20020045230A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA128
; CURRENT APPLICATION NUMBER: US/09/908,711
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US01/01360
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,867
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01344
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,888
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01329
; PRIOR FILING DATE: 2001-01-17

; SEQ ID NO 214915
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36094C.1.pap
US-10-424-599-214915

Query Match      39.1%; Score 50; DB 15; Length 78;
Best Local Similarity 61.1%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      2 TPDGGGGGQIGDNPLKA 19
      |||:|||||:
Db      40 TPKGGGGGPRGKNPPNKA 57

RESULT 11
US-10-437-963-149121
; Sequence 149121, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 149121
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49486C.1.pap
US-10-437-963-149121

Query Match      39.1%; Score 50; DB 16; Length 177;
Best Local Similarity 47.6%; Pred. No. 31;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      5 GQGGGQIGDNPLKMLKLA 25
      |||:|||||:
Db      19 GVGGGRLGQGSNEASRLAA 39

RESULT 12
US-10-425-115-231795
; Sequence 231795, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 231795
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
```

```

Query Match      37.9%; Score 48.5; DB 9; Length 365;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY      2  TPDQGGGGQIGDNPFLKAMEKL 23
      ||| : ||| ||| : :
Db      284  TPDKKGOTOI-PNPLLNIILRV 304

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 25, 2005, 20:02:44 ; Search time 14.1827 Seconds  
(without alignments)  
169.602 Million cell updates/sec

Title: DESAI-879\_116\_140  
Perfect score: 128  
Sequence: 1 ITPDGGGGQIGDNPLLKAMLKLI A 25  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	447	2	T18447
2	54	42.2	837	2	I57557
3	52	40.6	135	2	B49218
4	52	40.6	702	2	S48753
5	51	39.8	409	2	S04430
6	49.5	38.7	480	2	E75433
7	49	38.3	428	2	G71177
8	49	38.3	436	2	T46107
9	49	38.3	598	2	S66669
10	49	38.3	613	2	A56031
11	48	37.5	225	2	AF2140
12	47	36.7	435	2	T20152
13	47	36.7	1343	1	H64073
14	46.5	36.3	652	2	D82317
15	46.5	36.3	867	2	H70411
16	46	35.9	435	2	F84674
17	46	35.9	605	2	S01066
18	46	35.9	1134	2	D75014
19	45.5	35.5	161	2	T42006
20	45.5	35.5	694	2	S09794
21	45	35.2	206	2	JC2574
22	45	35.2	253	2	F86184
23	45	35.2	283	2	T19933
24	45	35.2	302	2	A84263
25	45	35.2	373	2	A56392
26	45	35.2	405	2	D97563
27	45	35.2	405	2	AD2784
28	45	35.2	509	2	D83651
29	45	35.2	532	2	A90037

30	45	35.2	576	2	T17842
31	45	35.2	664	1	VEHULA
32	45	35.2	665	2	S27267
33	45	35.2	665	2	S28182
34	45	35.2	1547	2	T13847
35	44	34.4	258	2	G72313
36	44	34.4	394	2	D69370
37	44	34.4	412	2	T32890
38	44	34.4	501	2	A11031
39	44	34.4	535	2	S44827
40	44	34.4	790	2	E48327
41	44	34.4	875	2	AE0401
42	44	34.4	890	2	F75289
43	43.5	34.0	415	2	S60078
44	43.5	34.0	415	2	B55563
45	43.5	34.0	754	2	S41391

## ALIGNMENTS

## RESULT 1

T18447  
HrpW protein - Erwinia amylovora  
C;Species: Erwinia amylovora  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18447  
R;Gaudriault, S.  
submitted to the EMBL Data Library, May 1998  
A;Reference number: Z18936  
A;Accession: T18447  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-447 <GAU>  
A;Cross-references: UNIPROT:O54508; EMBL:Y13831; NID:e1293450; PID:e1293451; PIDN:CAA74  
A;Experimental source: strain CFBP1430; specific host Pomoideae  
C;Genetics:  
A;Note: hrpW

Query Match 100.0%; Score 128; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 1e-11;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ITPDGGGGQIGDNPLLKAMLKLI A 25

DB 116 ITPDGGGGQIGDNPLLKAMLKLI A 140

## RESULT 2

I57557  
DNA-Binding Protein and transcription factor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I57557  
R;Quellie, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleveland, C.E.; Mol. Cell. Biol. 15, 3336-3343, 1995  
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosphatases  
A;Reference number: I57557; MUID:95280934; PMID:7760829  
A;Accession: I57557  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-837 <RES>  
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g1008876  
C;Genetics:  
A;Gene: STAT6  
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 42.2%; Score 54; DB 2; Length 837;

Best Local Similarity 64.3%; Pred. No. 5;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GCGGGQIGDNPLLK 18

|||||:|

Db 802 GEGGSLGSQLK 815

RESULT 3

B49218  
hemagglutinin homolog pMGAL.3 - Mycoplasma gallisepticum (fragment)  
C:Species: Mycoplasma gallisepticum  
C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B49218  
R:Markham, P.F.; Glew, M.D.; Whithear, K.G.; Walker, I.D.  
Infect. Immun. 61, 903-909, 1993  
A:Title: Molecular cloning of a member of the gene family that encodes pMGA, a hemagglutinin  
A:Reference number: A49218; MUID:93162830; PMID:8432610  
A:Accession: B49218  
A>Status: preliminary  
A:Molecule type: DNA; protein  
A:Residues: 1-135 <MAR>  
A:Cross-references: UNIPROT:Q53304; GB:855216; NID:g265625; PIDN:AA25398.1; PID:g265627  
A:Note: sequence extracted from NCBIN:125182, NCBIP:125184)  
C:Genetics:  
A:Genetic code: SGC3

Query Match 40.6%; Score 52; DB 2; Length 135;  
Best Local Similarity 64.3%; Pred. No. 1.3;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TPDGQGGQIGDNP 15  
| | | | |  
Db 57 TNPNGGGMGNDP 70

RESULT 4

S48753  
major surface protein (clone pMGAL.3) precursor - Mycoplasma gallisepticum  
C:Species: Mycoplasma gallisepticum  
C>Date: 01-Aug-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S48753  
R:Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.;  
FEBS Lett. 352, 347-352, 1994  
A:Title: The organisation of the multigene family which encodes the major cell surface protein  
A:Reference number: S48751; MUID:95010739; PMID:7925999  
A:Accession: S48753  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-702 <MAR>  
A:Cross-references: UNIPROT:Q49498; EMBL:L28424; NID:g535687; PIDN:AA62417.1; PID:g5356  
C:Genetics:  
A:Genetic code: SGC3  
A:Start codon: GTG

Query Match 40.6%; Score 52; DB 2; Length 702;  
Best Local Similarity 64.3%; Pred. No. 8.3;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TPDGQGGQIGDNP 15  
| | | | |  
Db 57 TNPNGGGMGNDP 70

RESULT 5

S04430  
translation elongation factor EF-Tu.A - Synecchococcus sp.  
C:Species: Synecchococcus sp.  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: S04430; G60663  
R:Meng, B.Y.; Shinozaki, K.; Suglura, M.  
Mol. Gen. Genet. 216, 25-30, 1989  
A:Title: Genes for the ribosomal proteins S12 and S7 and elongation factors EF-G and EF-  
A:Reference number: S04426; MUID:89281486; PMID:2499762  
A:Accession: S04430  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA

A:Residues: 1-409 <MEN>  
A:Cross-references: UNIPROT:P18668  
A:Note: the source is designated as Anacystis nidulans  
R:Ludwig, W.; Weizenegger, W.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenh  
Arch. Microbiol. 153, 241-247, 1990  
A:Title: Complete nucleotide sequences of seven subbacterial genes coding for the elonga  
A:Reference number: A60663; MUID:90240875; PMID:2110445  
A:Accession: G60663  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-324, 'D', 326-409 <LUD>  
C:Genetics:  
A:Gene: tufa

C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homol  
C:Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis  
F13-139/Domain: translation elongation factor Tu homology <ETU>  
F19-26/Region: nucleotide-binding motif A (P-loop)  
F136-139/Region: GTP-binding NXKD motif  
F174-176/Region: GTP-binding SAK/L motif  
F125,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #st

Query Match 39.8%; Score 51; DB 2; Length 409;  
Best Local Similarity 57.1%; Pred. No. 6.5;  
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 6 QGG--GQIGDNPFLKXKLI 24  
| | | | | : | | |  
Db 183 QGGAGQGDNPWDKILKLM 203

RESULT 6

E75433  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: E75433  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; M.  
S.; Smith, H.O.; Venster, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: E75433  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-480 <WHI>  
A:Cross-references: UNIPROT:Q9RV87; GB:AE001963; NID:g6458869; PIDN:AAF107  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR142  
A:Map position: 1  
C:Superfamily: Deinococcus radiodurans hypothetical protein DR142

Query Match 38.7%; Score 49.5; DB 2; Length 480;  
Best Local Similarity 60.0%; Pred. No. 13;  
Matches 12; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 5 GQGGGQIGD-NPLLKXKLI 23  
| | | | | : | | |  
Db 157 GQGGGALGDFAPLLAFRQL 176

RESULT 7

G71177  
hypothetical protein PH1701 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C:Accession: G71177  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
M.; Ofuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137; PMID:9679194

```
A;Accession: G71177
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-428 <RAW>
A;Cross-references: UNIPROT:O59360; GB:AP000007; PIDN:BAA30814.1; PID:G325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PHI701

Query Match      38.3%; Score 49; DB 2; Length 428;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GGGGQGNPLKAMKLL 23
      |||||:||||:|
Db      286 GAQSGDNAMLKAMHRL 301

RESULT 8
T46107
hypothetical protein T25B15.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46107
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23021
A;Accession: T46107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <ALC>
A;Cross-references: UNIPROT:Q9FT45; EMBL:AL132972
A;Experimental source: cultivar Columbia; BAC clone T25B15
C;Genetics:
A;Map position: 3
A;Introns: 418/1
A;Note: T25B15.140

Query Match      38.3%; Score 49; DB 2; Length 436;
Best Local Similarity 52.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      3 PDGGGGGQIGDNPPLKAML 21
      |||||:||||:|
Db      22 PDRPGSQINSNVLVALL 40

RESULT 9
S66669
potassium channel (Kv1.5) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66669
R;Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A;Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit
A;Reference number: S66669; MUID:96032538; PMID:7556635
A;Accession: S66669
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-598 <SAS>
A;Cross-references: UNIPROT:P50638; EMBL:D45025; NID:G1060972; PIDN:BAA08082.1; PID:d100
C;Superfamily: potassium channel protein drk1

Query Match      38.3%; Score 49; DB 2; Length 598;
Best Local Similarity 45.5%; Pred. No. 20;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy      3 PDGGGGGQIGDNPPLKAMKLLI 24
      |||||:||||:|
Db      366 PGGGGGGQGGQAMSLAILRVI 387
```

```
RESULT 10
A56031
potassium channel KCNA5 - human
N;Alternate names: potassium channel HK2; potassium channel PCN1; shaker-related potass
C;Species: Homo sapiens (man)
C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A56031; A38556; B39922; A38074
R;Phillipson, L.H.; LaMendola, J.; Bell, G.I.; Steiner, D.F.
submitted to GenBank, September 1990
A;Reference number: A56031
A;Accession: A56031
A;Molecule type: mRNA
A;Residues: 1-613 <PHI>
A;Cross-references: UNIPROT:P22460; GB:M55513; NID:gi189653; PIDN:AAA36422.1; PID:gi18965
R;Phillipson, L.H.; Hice, R.E.; Schaefer, K.; LaMendola, J.; Bell, G.I.; Nelson, D.J.; S
Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A;Title: Sequence and functional expression in Xenopus oocytes of a human inulinoma an
A;Reference number: A38556; MUID:91095456; PMID:1986382
A;Accession: A38556
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-56 'G', 58-137, 'L', 139-213, 'R', 215-227, 'P', 229-545, 'QG', 546-613 <PH2>
A;Cross-references: GB:M55513
R;Ramkun, M.M.; Knoth, K.M.; Walbridge, J.A.; Kroemer, H.; Roden, D.M.; Glover, D.M.
FASEB J. 5, 331-337, 1991
A;Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs
A;Reference number: A39922; MUID:91160866; PMID:2001794
A;Accession: B39922
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-54, 56-137, 'L', 139-186, 'G', 189-213, 'R', 215-227, 'P', 229-297, 'PTQRGH', 309-55
R;Curran, M.E.; Landes, G.M.; Keating, M.T.
Genomics 12, 729-737, 1992
A;Title: Molecular cloning, characterization, and genomic localization of a human potas
A;Reference number: A38074; MUID:92241872; PMID:1349297
A;Accession: A38074
A;Molecule type: DNA
A;Residues: 1-137, 'L', 139-153, 'R', 155-213, 'R', 215-227, 'P', 229-281, 'V', 283-578, 'QLPPREV'
A;Cross-references: GB:M83254; NID:gi90202; PIDN:AAA60146.1; PID:gi90203
A;Experimental source: heart
A;Note: sequence extracted from NCBI backbone (NCBIN:98573, NCBIP:98577)
C;Genetics:
A;Gene: GDB:KCNAS
A;Cross-references: GDB:127904; OMIM:176267
A;Map position: 12p13.33-12p13.31
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; vol
F;125,190/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;557/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match      38.3%; Score 49; DB 2; Length 613;
Best Local Similarity 45.5%; Pred. No. 21;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy      3 PDGGGGGQIGDNPPLKAMKLLI 24
      |||||:||||:|
Db      381 PGGGGGGQGGQAMSLAILRVI 402

RESULT 11
AF2140
hypothetical protein all2677 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2140
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
```

A; Cross-references: UNIKPOL:Q6RIN; G8:BA0000019;  
A; Experimental source: strain PCC 7120  
C: Genetics:  
A: Gene: all2677

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 03-Jul-2004  
C;Accession: D82317  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
l p b. Metalkanos, J.T.; Venter, J.C.; Fraser, C.M.

L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000  
A: Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
B: Reference number: A82035; PMID:20406833; PMID:10952301

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-652 <HRI>  
A;Cross-references: NID:G9654900; PIDN:AAR93  
A;Experimental source: serogroup O1; strain Ni961; biotype E1 Tor  
C;Genetics:  
A;Gene: VC0475  
A;Map position: 1

```

Query Match      36.3%; Score 46.5; DB 2; Length 652;
Best Local Similarity 61.9%; Pred. No. 54;
Matches 13; Conservative 1; Mismatches 4; Indels 3; Gaps 2;

Qy      1  ITPD-GO--GGGQIGDNPLLK  18
      :||| ||| ||| ||| |||
Db      428  VIFDWGVQVGGGNLYGNPDLK  448

RESULT 15

```

alanine-tRNA ligase (EC 6.1.1.7) - Aquifex aeolicus  
C.Species: Aquifex aeolicus  
C.Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C.Accession: H70411

Nature 392, 353-358, 1998  
Nature 397, 335-338, 1999  
Ridebeckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Granam, D.E.; V.  
Nature 392, 353-358, 1998

A:Accession: H70411  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-867 <AQF>  
A:Cross-references: UNIPROT:Q67323; GB:AE000733; NID:g2983720; PIDN:AAC07289.1; PID:g292222  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: alas  
C:Superfamily: alanyl-tRNA ligase  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 36.3%; Score 46.5; DB 2; Length 867;  
Best Local Similarity 47.6%; Pred. No. 73;  
Matches 10; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

QY 6 QGGGQIGDNPILL---KAMLKLL 23  
:|||||::|||:  
DB 495 EGGGQIGDAGIIESDKALPKV 515

Job time : 16.1827 secs

Search completed: January 25, 2005, 20:37:00  
Job time : 16.1827 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 19:58:54 ; Search time 79.0865 Seconds  
(without alignments)  
181.881 Million cell updates/sec

Title: DESAI-879\_116\_140  
Perfect score: 128  
Sequence: 1 ITPDGGGGQIGDNPLKAMKLIA 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02.4  
1: uniprot\_sprot.4  
2: uniprot\_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	447	2	O54508
2	128	100.0	447	2	O9LAW2
3	128	100.0	450	2	O6XDB8
4	128	100.0	450	2	AAQ17046
5	128	100.0	450	2	AAS45453
6	120	93.8	138	2	O79AW7
7	71	55.5	479	2	O6RKS2
8	71	55.5	479	2	O6D5C8
9	71	55.5	479	2	AAS20352
10	60	46.9	237	2	O873M4
11	57	44.5	174	2	O9P923
12	56	43.8	165	2	O9P920
13	54	42.2	172	2	O9P921
14	54	42.2	220	2	O74200
15	54	42.2	837	1	STA6 MOUSE
16	53	41.4	173	2	O9P919
17	52	40.6	133	2	O49469
18	52	40.6	135	2	O53304
19	52	40.6	210	1	SODM ASPFU
20	52	40.6	229	2	O6CFAL
21	52	40.6	584	2	O9KH13
22	52	40.6	692	2	O7NAN9
23	52	40.6	702	2	O49498
24	52	40.6	708	2	O7NAP2
25	52	40.6	710	2	O7NBR1
26	51	39.8	409	1	EFTU_SYNPF6
27	51	39.8	409	1	EFTU_SYNPF7
28	51	39.8	578	2	O7S389
29	51	39.8	667	2	O7NBR3
30	51	39.8	697	2	O7NBS5
31	50.5	39.5	504	2	O6BXD4

32 50.5 39.5 891 2 Q7VOG3  
33 50 39.1 61 2 P70383  
34 50 39.1 177 2 Q9FTW3  
35 50 39.1 889 1 SYA\_SYNXP  
36 50 39.1 892 2 Q7VEG5  
37 50 39.1 1759 2 Q73XY5  
38 50 39.1 1759 2 AAS04490  
39 49.5 38.7 97 2 Q8LOW7  
40 49.5 38.7 480 2 Q9RV87  
41 49.5 38.7 962 2 Q8DIY4  
42 49 38.3 428 2 O59360  
43 49 38.3 436 2 O9FT45  
44 49 38.3 452 2 Q7RV58  
45 49 38.3 593 2 Q28248

#### ALIGNMENTS

#### RESULT 1

O54508 PRELIMINARY; PRT; 447 AA.  
AC O54508;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW protein.  
DE HrpW protein.  
GN Names=hrpW;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CPBP1430;  
RX MEDLINE=98086111; PubMed=9426142;  
RA Gaudriault S., Malandrin L., Paulin J.P., Barny M.A.;  
RT "DepA, an essential pathogenicity factor of Erwinia amylovora showing  
RT homology with AvrE of Pseudomonas syringae, is secreted via the Hrp  
RT secretion pathway in a DapB-dependent way.";  
RL Mol. Microbiol. 26:1057-1069(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CPBP1430;  
RX MEDLINE=98316710; PubMed=9654138;  
RA Gaudriault S., Brisset M.N., Barny M.A.;  
RT "HrpW of Erwinia amylovora, a new Hrp-secreted protein.";  
RL FEBS Lett. 428:224-228(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EA321;  
RX Kim J.F., Zumoff C.H., Beer S.V.;  
RT "HrpW, a new harpin of Erwinia amylovora, is a member of a family of  
RT pectate lyases.";  
RL Phytopathology 87:0-0(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EA321;  
RX MEDLINE=98422475; PubMed=9748455;  
RA Kim J.F., Beer S.V.;  
RT "HrpW of Erwinia amylovora, a new harpin that contains a domain  
RT homologous to pectate lyases of a distinct class.";  
RL J. Bacteriol. 180:5203-5210(1998).  
DR EMBL; Y13831; CAA74158.1; -;  
DR EMBL; U94513; AAC62314.1; -;  
DR PIR; T18447; T18447.  
DR HSP; Q9RHW0; IEE6.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0030570; F:pectate lyase activity; IEA.  
DR InterPro; IPR011050; Pectin\_lyas\_like.  
DR InterPro; IPR004898; Pect\_lyase.  
DR Pfam; PF03211; Pectate\_lyase; 1.  
SQ SEQUENCE 447 AA; 45347 MW; 7A744D169D6D9CF3 CRC64;

Q7VQG3 candidatus  
P70383 mus musculus  
Q9FTW3 oryza sativ  
Q7U3R9 synchococc  
Q7VEG5 prochloroc  
Q73XY5 mycobacteri  
AAS04490 mycobacte  
Q8LOW7 vibrio para  
Q9RV87 deinococcu  
Q8DIY4 synchococc  
O59360 pyrococcus  
Q9FT45 arabidopsis  
Q7RV58 neurospora  
Q28248 canis famil

DR InterPro: IPR011050; Pectin lyas\_like.  
DR InterPro: IPR004898; Pect lyase.  
DR Pfam: PF03211; Pectate lyase; 1.  
SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;  
  
Query Match 100.0%; Score 128; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 5.5e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ITPDGGGGGQIGDNPPLKAMKLIA 25  
DB 114 ITPDGGGGGQIGDNPPLKAMKLIA 138  
  
RESULT 4  
AAQ17046 PRELIMINARY; PRT; 450 AA.  
AC AAQ17046;  
DT 03-MAR-2004 (TrEMBLrel. 27, Created)  
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW.  
GN Erwinia pyrifoliae.  
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=79967;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WT#3;  
RA Shrestha R., Baek S.J., Cho J.M., Park D.H., Hwang I.K.,  
RA Hur J.H., Lim C.K.;  
RT "Molecular characterization of hrp genes cluster of Erwinia pyrifoliae  
RT and expression of hrpE encoding elicitor of the hypersensitive  
RT response";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY237642; AAQ17046.1; -.  
SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;  
  
Query Match 100.0%; Score 128; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 5.5e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ITPDGGGGGQIGDNPPLKAMKLIA 25  
DB 114 ITPDGGGGGQIGDNPPLKAMKLIA 138  
  
RESULT 5  
AAS45453 PRELIMINARY; PRT; 450 AA.  
ID AAS45453  
AC AAS45453;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW.  
GN Erwinia pyrifoliae.  
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=79967;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WT#3;  
RA Shrestha R., Baek S.J., Park D.H., Bae H.N., Cho J.M., Hwang I.,  
RA Hur J.H., Lim C.K.;  
RT "Identification of hrp genes cluster and characterization of HR  
RT elicitor hrpNEP gene in Erwinia pyrifoliae";  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY530755; AAS45453.1; -.  
SQ SEQUENCE 450 AA; 45509 MW; 085F90CD322C3A74 CRC64;  
  
Query Match 100.0%; Score 128; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 5.5e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 128; DB 2; Length 447;  
Best Local Similarity 100.0%; Pred. No. 5.4e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ITPDGGGGGQIGDNPPLKAMKLIA 25  
DB 116 ITPDGGGGGQIGDNPPLKAMKLIA 140  
  
RESULT 2  
Q9LAW2 PRELIMINARY; PRT; 447 AA.  
ID Q9LAW2  
AC Q9LAW2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Harpin HrpW.  
GN Name=hrpW;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ea246;  
RA Kim J.F., Laby R.J., Beer S.V.;  
RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF083620; AAF63402.1; -.  
DR HSP; Q9RHW0; 1EE6.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:00030570; F:pectate lyase activity; IEA.  
DR InterPro: IPR011050; Pectin lyas\_like.  
DR InterPro: IPR004898; Pect lyase.  
DR Pfam: PF03211; Pectate lyase; 1.  
SQ SEQUENCE 447 AA; 45340 MW; 08BAEA3871EDC2F6 CRC64;  
  
Query Match 100.0%; Score 128; DB 2; Length 447;  
Best Local Similarity 100.0%; Pred. No. 5.4e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ITPDGGGGGQIGDNPPLKAMKLIA 25  
DB 116 ITPDGGGGGQIGDNPPLKAMKLIA 140  
  
RESULT 3  
Q6XDB8 PRELIMINARY; PRT; 450 AA.  
ID Q6XDB8  
AC Q6XDB8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HrpW.  
GN Name=hrpW;  
OS Erwinia pyrifoliae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=79967;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WT#3;  
RA Shrestha R., Baek S.J., Bae H.N., Cho J.M., Park D.H., Hwang I.K.,  
RA Hur J.H., Lim C.K.;  
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
RL [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=WT#3;  
RA Shrestha R., Baek S.J., Park D.H., Bae H.N., Cho J.M., Hwang I.,  
RA Hur J.H., Lim C.K.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY237642; AAQ17046.1; -.  
DR EMBL; AY530755; AAS45453.1; -.  
  
Query Match 100.0%; Score 128; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 5.5e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 5.5e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPFLKAMKLI 25  
Db 114 ITPDGGGGQIGDNPFLKAMKLI 138  
|||||

RESULT 6  
Q79AW7 PRELIMINARY; PRT; 138 AA.  
AC Q79AW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE HrpW (fragment).  
GN Name=hrpW;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ea321;  
RX MEDLINE=98115919; PubMed=9448330;  
RA Bogdanove A.J., Kim J.F., Wei Z., Kolchinsky P., Charkowski A.O.,  
RA Conlin A.K., Collmer A., Beer S.V.;  
RT "Homology and functional similarity of an hrp-linked pathogenicity  
RT locus, *dapEF*, of *Erwinia amylovora* and the avirulence locus *avrE* of  
RT *Pseudomonas syringae* pathovar *tomato*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:1325-1330 (1998).  
DR EMBL; U97504; AAC04849.1; -;  
FT NON TER 138 138  
SQ SEQUENCE 138 AA; 13788 MW; 4FE177177C74B3C6 CRC64;

Query Match 93.8%; Score 120; DB 2; Length 138;  
Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPFLKAMKLI 23  
Db 116 ITPDGGGGQIGDNPFLKAMKLI 138  
|||||

RESULT 7  
Q6RK52 PRELIMINARY; PRT; 479 AA.  
AC Q6RK52;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE HrpW.  
GN Name=hrpW;  
OS Pectobacterium atrosepticum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SCRI1039;  
RA Holeva M.C., Bell K.S., Hyman L.J., Avrova A.O., Whisson S.C.,  
RA Birch P.R.J., Toth I.K.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY496066; AAS20352.1; -;  
DR InterPro; IPR011050; Pectin\_lyase\_like.  
DR InterPro; IPR004898; Pect. lyase.  
DR Pfam; PF03211; Pectate\_lyase; 1.  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

Query Match 55.5%; Score 71; DB 2; Length 479;  
Best Local Similarity 58.3%; Pred. No. 0.12;  
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPFLKAMKLI 24  
Db 166 INPTADGGGQSGNDLLKALLELI 189  
|||||

RESULT 8  
Q6D5C8 PRELIMINARY; PRT; 479 AA.  
AC Q6D5C8;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Type III effector protein.  
GN Name=hrpW; ORFNames=ECA2112;  
OS Erwinia carotovora subsp. atroseptica SCRI1043.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=218491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SCRI1043;  
RA Bell K.S., Sebaihia M., Pritchard L., Holden M., Hyman L.J.,  
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,  
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,  
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,  
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,  
RA Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX950851; CAG75014.1; -;  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

Query Match 55.5%; Score 71; DB 2; Length 479;  
Best Local Similarity 58.3%; Pred. No. 0.12;  
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPFLKAMKLI 24  
Db 166 INPTADGGGQSGNDLLKALLELI 189  
|||||

RESULT 9  
AAS20352 PRELIMINARY; PRT; 479 AA.  
AC AAS20352;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DE HrpW.  
GN HRPW.  
OS Pectobacterium atrosepticum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SCRI1039;  
RA Holeva M.C., Bell K.S., Hyman L.J., Avrova A.O., Whisson S.C.,  
RA Birch P.R.J., Toth I.K.;  
RT "Rapid demonstration of a role early in disease development for the  
RT type III secretion system of *Erwinia carotovora* subsp. *atroseptica*  
RT SCRI1039 using a pooled transposon mutation grid.";  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY496066; AAS20352.1; -;  
SQ SEQUENCE 479 AA; 46706 MW; 3463E226CDF0406A CRC64;

Query Match 55.5%; Score 71; DB 2; Length 479;  
Best Local Similarity 58.3%; Pred. No. 0.12;  
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPFLKAMKLI 24  
Db 166 INPTADGGGQSGNDLLKALLELI 189  
|||||

```

RESULT 10
Q973M4 PRELIMINARY; PRT; 237 AA.
AC Q973M4; 2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Manganese superoxide dismutase (Fragment).
DE Name=MnSOD;
GN Malassezia sympodialis.
OS Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Exobasidiomycetidae; Malasseziales; Malassezia.
OX NCBI_TaxID=76777;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson A., Rasool O., Schmidt M., Kodzius R., Cramer R.,
RA Scheynius A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR EMBL; AJ548421; CAD68071.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; Sod_Fe_C; 1.
DR Pfam; PF00081; Sod_Fe_N; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
FT NON_TER 1
FT SEQUENCE 237 AA; 26716 MW; 6C2096462E8402E9 CRC64;
SQ
Query Match 46.9%; Score 60; DB 2; Length 237;
Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKMLK 22
DB 118 WAPQSGGGQLNDGFLKQAIDK 139

RESULT 11
Q9P923 PRELIMINARY; PRT; 174 AA.
AC Q9P923; 2003 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Manganese-dependent superoxide dismutase (EC 1.15.1.1)
DE (Fragment).
DE Name=soda;
GN Pneumocystis carinii f. sp. muris.
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=42066;
RN [1]
RP SEQUENCE FROM N.A.
RA Denis C.M., Mazars E., Guyot K., Oberg-Ferragut C., Viscogliosi E.,
RA Dei-Cas E., Wakefield A.E.;
RL "Genetic divergence at the SODA locus of six different formae
RT specialies of Pneumocystis carinii.";
RL Med. Mycol. 38:289-300(2000).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR EMBL; AF146754; AAP25726.1; -.
DR HSP; Q92450; IKKC.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; Sod_Fe_C; 1.
DR Pfam; PF00081; Sod_Fe_N; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
FT NON_TER 1
FT SEQUENCE 174 AA; 20198 MW; 2730D8F435576124 CRC64;
SQ
Query Match 44.5%; Score 57; DB 2; Length 174;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ITPDGGGGGQIGDNPFLKMLK 22
DB 71 LLPNKGQGGQLINGFLVEAIKK 92

RESULT 12
Q9P920 PRELIMINARY; PRT; 165 AA.
AC Q9P920; 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Manganese-dependent superoxide dismutase (EC 1.15.1.1)
DE (Fragment).
DE Name=soda;
GN Pneumocystis carinii f. sp. macaca.
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=112250;
RN [1]
RP SEQUENCE FROM N.A.
RA Denis C.M., Mazars E., Guyot K., Oberg-Ferragut C., Viscogliosi E.,
RA Dei-Cas E., Wakefield A.E.;
RL "Genetic divergence at the SODA locus of six different formae
RT specialies of Pneumocystis carinii.";
RL Med. Mycol. 38:289-300(2000).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR EMBL; AF146754; AAP25726.1; -.
DR HSP; Q92450; IKKC.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; Sod_Fe_C; 1.
DR Pfam; PF00081; Sod_Fe_N; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
FT NON_TER 1
FT SEQUENCE 165 AA; 19178 MW; 4C01F3C7C48D514E CRC64;
SQ
Query Match 43.8%; Score 56; DB 2; Length 165;
Best Local Similarity 50.0%; Pred. No. 5.9;

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Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPPLKAMLK 22
: | : ||||| : ||: | :
Db 62 LLPPKGGGGQIFDGPLVDAIKK 83

RESULT 13
Q9P921 PRELIMINARY; PRT; 172 AA.
AC Q9P921;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Manganese-dependent superoxide dismutase (SC 1.15.1.1)
GN (Fragment).
DN Name=soda;
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OC NCBI_TaxID=42068;
RN [1]
RP SEQUENCE FROM N.A.
RA Denis C.M., Mazars E., Guyot K., Odberg-Ferragut C.,
RA Dei-Cas E., Wakefield A.E.;
RT "Genetic divergence at the SODA locus of six different formae
RT speciales of Pneumocystis carinii.";
RL Med. Mycol. 38:289-300(2000).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
EMBL; AF146753; AAF25725.1; -.
HSSP; Q92450; 1KKC.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004784; F:superoxide dismutase activity; IEA.
GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IPR001189; SODismutase.
PFam; PF02777; Sod_Fe_C; 1.
PFam; PF00081; Sod_Fe_N; 1.
PRINTS; PR01703; MNSODISMUTASE.
PRODOM; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD_MN; 1.
NON_TER 1 172
NON_TER 172 172
SEQUENCE 172 AA; DB 2; Length 172;
Query Match 42.2%; Score 54; DB 2; Length 172;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPPLKAMLK 22
: | : ||||| : ||: | :
Db 69 LLPPKGGGGQIFDGPLVDAIKK 90

RESULT 14
O74200 PRELIMINARY; PRT; 220 AA.
ID O74200
AC O74200;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Manganese superoxide dismutase precursor.
GN Name=mnsod;
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OC NCBI_TaxID=4754;

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[1]
RN SEQUENCE FROM N.A.
RP Denis C.M., Guyot K., Dei-Cas E., Camus D., Odberg-Ferragut C.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
EMBL; AF036321; AAC24764.1; -.
HSSP; Q92450; 1KKC.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004784; F:superoxide dismutase activity; IEA.
GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR001189; SODismutase.
PFam; PF02777; Sod_Fe_C; 1.
PFam; PF00081; Sod_Fe_N; 1.
PRINTS; PR01703; MNSODISMUTASE.
PRODOM; PD000475; SODismutase; 1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
PROSITE; PS00088; SOD_MN; 1.
Oxidoreductase; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 48 169 manganese superoxide dismutase.
FT CHAIN 170 183 manganese superoxide dismutase.
FT CHAIN 184 207 manganese superoxide dismutase.
FT CHAIN 208 220 manganese superoxide dismutase.
FT CHAIN 28 35 manganese superoxide dismutase.
FT CHAIN 36 47 manganese superoxide dismutase.
SQ SEQUENCE 220 AA; 25869 MW; 73B1P11C98929E18 CRC64;

Query Match 42.2%; Score 54; DB 2; Length 220;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ITPDGGGGQIGDNPPLKAMLK 22
: | : ||||| : ||: | :
Db 106 LLPNKGGGGIINGPLVEAIKK 127

RESULT 15
STA6 MOUSE
ID STA6 MOUSE STANDARD; PRT; 837 AA.
AC P52633;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and transcription activator 6.
GN Name=Stat6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95280934; PubMed=7760829;
RA Queller F.W., Shimoda K., Thierfelder W., Fischer C.L., Kim A.,
RA Ruben S.M., Cleveland J.L., Pierce J.H., Keegan A.D., Nelms K.,
RA Paul W.E., Ihle J.N.;
RT "Cloning of murine Stat6 and human Stat6, Stat proteins that are
RT tyrosine phosphorylated in responses to IL-4 and IL-3 but are not
RT required for mitogenesis.";
RL Mol. Cell. Biol. 15:3336-3343(1995).
CC -1- FUNCTION: Carries out a dual function: signal transduction and
CC activation of transcription. Involved in interleukin-4 signalling.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -1- PTM: Tyrosine phosphorylated following stimulation by IL-4 and IL-
CC 3.

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Wed Jan 26 08:08:25 2005

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CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC -----
CC EMBL; L47650; AAA79006.1; -.
CC PIR; I57557; I57557.
CC HSP; P42227; IBG1.
CC MGD; MGI:103034; Stat6.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0042127; P:regulation of cell proliferation; IDA.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC InterPro; IPR001217; STAT.
CC InterPro; IPR000980; SH2.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF01017; STAT_alpha; 1.
CC Pfam; PF02864; STAT_bind; 1.
CC Pfam; PF02865; STAT_int; 1.
CC SMART; SM00252; SH2; 1.
CC PROSITE; PS00001; SH2; 1.
CC Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 517 632 SH2.
FT MOD_RES 641 641 Phosphotyrosine (by JAK) (By similarity).
SQ SEQUENCE 837 AA; 93725 MW; FD7D7C448743EFC7 CRC64;

Query Match 42.2%; Score 54; DB 1; Length 837;
Best Local Similarity 64.3%; Pred. No. 64;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 GCGGGQIGDNPLK 18
DB 802 GCGGSLGSGPLK 815
|:|:|:|:|
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Search completed: January 25, 2005, 20:35:55  
Job time : 80.0865 secs